

part  
A

Tue Jul 17 14:16:55 2001 [BLASTN 2.1.3 [Apr-1-2001], NCBI]  
 /home/ruby/va/Molbio/carpenda/temp1/ss.DNA40981 (2906 bp)

Sequences producing High-scoring Segment Pairs:

		Frame	Score	Match	Pct	E-val
1	P_AAC97475	Human angiogenesis-associated protein PR	+	2906	2906	100 0.0
2	P_AAF44261	Human PRO331 nucleotide sequence SEQ ID	+	2906	2906	100 0.0
3	P_AAF72423	Human PRO331 cDNA.	+	2906	2906	100 0.0
4	P_AAZ52207	Human PRO331 protein encoding cDNA, UNQ2	+	2906	2906	100 0.0
5	P_AAA77596	Human PRO331 cDNA sequence SEQ ID NO:106	+	2906	2906	100 0.0
6	P_AAX52265	Protein PRO331 cDNA clone DNA40981-1234.	+	2906	2906	100 0.0
7	AX098385	Sequence 11 from Patent WO0119991.	+	2906	2906	100 0.0
8	AB046800	Homo sapiens mRNA for KIAA1580 protein,	+	2889	2898	100 0.0
9	AC021820	Homo sapiens clone RP11-40H19, WORKING D	+	2136	2136	100 0.0
10	AC080100	Homo sapiens chromosome 11 clone RP11-45	-	2132	2135	100 0.0

>1 P\_AAC97475 Human angiogenesis-associated protein PRO331 cDNA, SEQ ID NO:136.  
 (2906 bp) [1 seg]

Score = 2906 (5761 bits), Expect = 0.0

Identities = 2906/2906 (100%), at 1,1-2906,2906, Strand +/-

DNA40981 1 GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTTTGGTGGTGGCTGTTGGG  
 \*\*\*\*\*  
 P\_AAC97475 1 GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTTTGGTGGTGGCTGTTGGG  
 \*\*\*\*\*  
 DNA40981 61 TGCCTTGCAAAATGAAGGATGCAGGACGCAGCTTCCTGGAACCGAACGCAATGGAT  
 \*\*\*\*\*  
 P\_AAC97475 61 TGCCTTGCAAAATGAAGGATGCAGGACGCAGCTTCCTGGAACCGAACGCAATGGAT  
 \*\*\*\*\*  
 DNA40981 121 AACTGATTGTCAAGAGAGAAGGAAGAACGAAGCTTTCTTGTGAGCCCTGGATCTTA  
 \*\*\*\*\*  
 P\_AAC97475 121 AACTGATTGTCAAGAGAGAAGGAAGAACGAAGCTTTCTTGTGAGCCCTGGATCTTA  
 \*\*\*\*\*  
 DNA40981 181 ACACAAATGTGTATATGTGCACACAGGGAGCATTCAAGAATGAAATAAACAGAGTTAGA  
 \*\*\*\*\*  
 P\_AAC97475 181 ACACAAATGTGTATATGTGCACACAGGGAGCATTCAAGAATGAAATAAACAGAGTTAGA  
 \*\*\*\*\*  
 DNA40981 241 CCCGCGGGGGTTGGTGTGTTCTGACATAAATAATCTTAAAGCAGCTGTTCCCCCTCC  
 \*\*\*\*\*  
 P\_AAC97475 241 CCCGCGGGGGTTGGTGTGTTCTGACATAAATAATCTTAAAGCAGCTGTTCCCCCTCC  
 \*\*\*\*\*  
 DNA40981 301 CCACCCCCAAAAAAAGGATGATTGGAAATGAAGAACCGAGGATTCACAAAGAAAAAGT  
 \*\*\*\*\*  
 P\_AAC97475 301 CCACCCCCAAAAAAAGGATGATTGGAAATGAAGAACCGAGGATTCACAAAGAAAAAGT  
 \*\*\*\*\*  
 DNA40981 361 ATGTTCATTTCTCTATAAAGGAGAAAGTGAGCCAAGGAGATATTTTGAATGAAAAG  
 \*\*\*\*\*  
 P\_AAC97475 361 ATGTTCATTTCTCTATAAAGGAGAAAGTGAGCCAAGGAGATATTTTGAATGAAAAG  
 \*\*\*\*\*  
 DNA40981 421 TTTGGGGCTTTTAGTAAAGTAAAGAACCTGGTGTGGTGGTTCTTCTTTGAA  
 \*\*\*\*\*  
 P\_AAC97475 421 TTTGGGGCTTTTAGTAAAGTAAAGAACCTGGTGTGGTGGTTCTTCTTTGAA  
 \*\*\*\*\*  
 DNA40981 481 TTTCCCACAAGAGGGAGGGAAATTATAATACATCTGCAAAGAAATTCAAGAGAAGAAA  
 \*\*\*\*\*  
 P\_AAC97475 481 TTTCCCACAAGAGGGAGGGAAATTATAATACATCTGCAAAGAAATTCAAGAGAAGAAA  
 \*\*\*\*\*  
 DNA40981 541 GTTGACCGCGGCAGATTGAGGCATTGATTGGGGAGAGAACCGAGCACAGTTGGA  
 \*\*\*\*\*  
 P\_AAC97475 541 GTTGACCGCGGCAGATTGAGGCATTGATTGGGGAGAGAACCGAGCACAGTTGGA  
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 DNA40981 601 TTTGTGCCTATGTTGACTAAAATTGACGGATAATTGCAGTTGGATTTCTTCATCAACC

BLAST RESULTS A-1

BLAST RESULTS A-2

P_AAC97475	601	***** TTTGTGCCTATGTTGACTAAAATTGACGGATAATTGCAAGTTGGATTTCATCAACC
DNA40981	661	***** TCCTTTTTAAATTTTATCCTTTGGTATCAAGATCATGCCTTCTCTGTCTT
P_AAC97475	661	***** TCCTTTTTAAATTTTATCCTTTGGTATCAAGATCATGCCTTCTCTGTCTT
DNA40981	721	***** AACCACCTGGATTCATCTGGATGTTGCTGTGATCAGTCTGAAATACAACGTGTTGAAT
P_AAC97475	721	***** AACCACCTGGATTCATCTGGATGTTGCTGTGATCAGTCTGAAATACAACGTGTTGAAT
DNA40981	781	***** TCCAGAAGGACCAACACCAGATAAATTATGAATGTTGAACAAAGATGACCTTACATCCACA
P_AAC97475	781	***** TCCAGAAGGACCAACACCAGATAAATTATGAATGTTGAACAAAGATGACCTTACATCCACA
DNA40981	841	***** GCAGATAATGATAGGTCCCTAGGTTAACAGGGCCCTATTGACCCCTGTTGTGGTGCT
P_AAC97475	841	***** GCAGATAATGATAGGTCCCTAGGTTAACAGGGCCCTATTGACCCCTGTTGTGGTGCT
DNA40981	901	***** GCTGGCTTCAACTTCTTGTGGTGGCTGGCTGGCTGGCGGGCTCAGACCTGCCCTCTGT
P_AAC97475	901	***** GCTGGCTTCAACTTCTTGTGGTGGCTGGCTGGCGGGCTCAGACCTGCCCTCTGT
DNA40981	961	***** GTGCTCTGCAGCAACCAGTTCAGCAAGGTGATTGTTGAGGT
P_AAC97475	961	***** GTGCTCTGCAGCAACCAGTTCAGCAAGGTGATTGTTGAGGT
DNA40981	1021	***** TCCGGATGGCATCTCACCAACACACGGCTGCTGAACCTCCATGAGAACCAAATCCAGAT
P_AAC97475	1021	***** TCCGGATGGCATCTCACCAACACACGGCTGCTGAACCTCCATGAGAACCAAATCCAGAT
DNA40981	1081	***** CATCAAAGTGAACAGCTTCAAGCACTTGAGGCACCTGGAAATCCTACAGTTGAGTAGGAA
P_AAC97475	1081	***** CATCAAAGTGAACAGCTTCAAGCACTTGAGGCACCTGGAAATCCTACAGTTGAGTAGGAA
DNA40981	1141	***** CCATATCAGAACCAATTGAAATTGGGGCTTCAATGGCTGGCGAACCTCAACACTCTGGA
P_AAC97475	1141	***** CCATATCAGAACCAATTGAAATTGGGGCTTCAATGGCTGGCGAACCTCAACACTCTGGA
DNA40981	1201	***** ACTCTTGACAATCGTCTTACTACCATCCGAATGGAGCTTGTATACTGTCTAAACT
P_AAC97475	1201	***** ACTCTTGACAATCGTCTTACTACCATCCGAATGGAGCTTGTATACTGTCTAAACT
DNA40981	1261	***** GAAGGAGCTGGTGCAGAACACCCCCATTGAAAGCATCCCTTATGCTTTAACAG
P_AAC97475	1261	***** GAAGGAGCTGGTGCAGAACACCCCCATTGAAAGCATCCCTTATGCTTTAACAG
DNA40981	1321	***** AATTCTTCTTGCGCCGACTAGACTTAGGGAAATTGAAAAGACTTACATCTCAGA
P_AAC97475	1321	***** AATTCTTCTTGCGCCGACTAGACTTAGGGAAATTGAAAAGACTTACATCTCAGA
DNA40981	1381	***** AGGTGCCTTGAAGGTCTGTCCAACCTGAGGTATTGAACCTGCCATGTGCAACCTCG
P_AAC97475	1381	***** AGGTGCCTTGAAGGTCTGTCCAACCTGAGGTATTGAACCTGCCATGTGCAACCTCG
DNA40981	1441	***** GGAAATCCCTAACCTCACACCGCTCATAAAACCTAGATGAGCTGGATCTTCTGGGAATCA
P_AAC97475	1441	***** GGAAATCCCTAACCTCACACCGCTCATAAAACCTAGATGAGCTGGATCTTCTGGGAATCA
DNA40981	1501	***** TTTATCTGCCATCAGGCCTGGCTTTCCAGGGTTGATGCACCTCAAAAACGTGGAT
P_AAC97475	1501	***** TTTATCTGCCATCAGGCCTGGCTTTCCAGGGTTGATGCACCTCAAAAACGTGGAT
DNA40981	1561	GATACAGTCCCAGATTCAAGTGATTGAACGGAATGCCATTGACAACCTCAGTCAGT

P_AAC97475	1561	GATACTCCCAGATTCAAGTGATTGAACGGAATGCCCTTGACAACCTCAGTCACTAGT
DNA40981	1621	GGAGATCAACCTGGCACACAATAATCTAACATTACTGCCTCATGACCTCTTCACTCCCTT
P_AAC97475	1621	GGAGATCAACCTGGCACACAATAATCTAACATTACTGCCTCATGACCTCTTCACTCCCTT
DNA40981	1681	GCATCATCTAGAGCGGATACATTTACATCACAAACCTTGGAACTGTAACTGTGACATACT
P_AAC97475	1681	GCATCATCTAGAGCGGATACATTTACATCACAAACCTTGGAACTGTAACTGTGACATACT
DNA40981	1741	GTGGCTCAGCTGGTGATAAAAGACATGGCCCCCTCGAACACAGCTGTTGTGCCCGGTG
P_AAC97475	1741	GTGGCTCAGCTGGTGATAAAAGACATGGCCCCCTCGAACACAGCTGTTGTGCCCGGTG
DNA40981	1801	TAACACTCCTCCCAATCTAAAGGGGAGGTACATTGGAGAGCTGACCAGAATTACTTCAC
P_AAC97475	1801	TAACACTCCTCCCAATCTAAAGGGGAGGTACATTGGAGAGCTGACCAGAATTACTTCAC
DNA40981	1861	ATGCTATGCTCCGGTGATTGTGGAGCCCCCTGCAGACCTCAATGTCACTGAAGGCATGGC
P_AAC97475	1861	ATGCTATGCTCCGGTGATTGTGGAGCCCCCTGCAGACCTCAATGTCACTGAAGGCATGGC
DNA40981	1921	AGCTGAGCTGAAATGTCGGGCCTCCACATCCCTGACATCTGTATCTGGATTACTCCAAA
P_AAC97475	1921	AGCTGAGCTGAAATGTCGGGCCTCCACATCCCTGACATCTGTATCTGGATTACTCCAAA
DNA40981	1981	TGGAACAGTCATGACACATGGGGCGTACAAAGTGCAGGATAGCTGTGCTCAGTGATGGTAC
P_AAC97475	1981	TGGAACAGTCATGACACATGGGGCGTACAAAGTGCAGGATAGCTGTGCTCAGTGATGGTAC
DNA40981	2041	GTTAAATTCAAAATGTAACGTGCAAGATAACAGGCATGTACACATGTATGGTGAGTAA
P_AAC97475	2041	GTTAAATTCAAAATGTAACGTGCAAGATAACAGGCATGTACACATGTATGGTGAGTAA
DNA40981	2101	TTCCGTTGGGAATACTACTGCTTCAGCCACCCCTGAATGTTACTGCAGCAACCAACTACTCC
P_AAC97475	2101	TTCCGTTGGGAATACTACTGCTTCAGCCACCCCTGAATGTTACTGCAGCAACCAACTACTCC
DNA40981	2161	TTTCTCTTACTTTCAACCGTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGCACG
P_AAC97475	2161	TTTCTCTTACTTTCAACCGTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGCACG
DNA40981	2221	GACCACAGATAACAAATGTGGTCCCCTCCAGTGGTCAGTGGGAGACCACCAATGTGAC
P_AAC97475	2221	GACCACAGATAACAAATGTGGTCCCCTCCAGTGGTCAGTGGGAGACCACCAATGTGAC
DNA40981	2281	CACCTCTCTCACACCAACAGAGCACAAGGTCGACAGAGAAAACCTTCACCATCCCAGTGAC
P_AAC97475	2281	CACCTCTCTCACACCAACAGAGCACAAGGTCGACAGAGAAAACCTTCACCATCCCAGTGAC
DNA40981	2341	TGATATAAACAGTGGGATCCCAAGGAATTGATGAGGTCATGAAGACTACCAAAATCATCAT
P_AAC97475	2341	TGATATAAACAGTGGGATCCCAAGGAATTGATGAGGTCATGAAGACTACCAAAATCATCAT
DNA40981	2401	TGGGTGTTGTGCCATCACACTCATGGCTGCAGTGATGCTGGTCATTTCTACAAGAT
P_AAC97475	2401	TGGGTGTTGTGCCATCACACTCATGGCTGCAGTGATGCTGGTCATTTCTACAAGAT
DNA40981	2461	GAGGAAGCAGCACCATCGGAAAACCATCACGCCCAACAAGGACTGTTGAAATTATTAA
P_AAC97475	2461	GAGGAAGCAGCACCATCGGAAAACCATCACGCCCAACAAGGACTGTTGAAATTATTAA
DNA40981	2521	TGTGGATGATGAGATTACGGGAGACACACCCATGGAAAGCCACCTGCCATGCCTGCTAT

BLAST RESULTS A-4

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P_AAC97475 2521 TGTGGATGATGAGATTACGGGAGACACACCCATGGAAAGCCACCTGCCCATGCCTGCTAT
DNA40981 2581 CGAGCATGAGCACCTAAACTACAATCATAACTACAAATCTCCCTCAACCACACAAC
*****
P_AAC97475 2581 CGAGCATGAGCACCTAAACTACAATCATAACTACAAATCTCCCTCAACCACACAAC
DNA40981 2641 AGTTAACACAATAAATTCAATACACAGTCAGTGCATGAACCGTTATTGATCCGAATGAA
*****
P_AAC97475 2641 AGTTAACACAATAAATTCAATACACAGTCAGTGCATGAACCGTTATTGATCCGAATGAA
DNA40981 2701 CTCTAAAGACAATGTACAAGAGACTCAAATCTAAAACATTTACAGAGTTACAAAAAACAA
*****
P_AAC97475 2701 CTCTAAAGACAATGTACAAGAGACTCAAATCTAAAACATTTACAGAGTTACAAAAAACAA
DNA40981 2761 ACAATCAAAAAAAAGACAGTTATTAAAAATGACACAAATGACTGGGCTAAATCTACTG
*****
P_AAC97475 2761 ACAATCAAAAAAAAGACAGTTATTAAAAATGACACAAATGACTGGGCTAAATCTACTG
DNA40981 2821 TTTCAAAAAAGTGTCTTACAAAAAACAAAAAGAAAAGAAATTATTATTAAAAATT
*****
P_AAC97475 2821 TTTCAAAAAAGTGTCTTACAAAAAACAAAAAGAAAAGAAATTATTATTAAAAATT
DNA40981 2881 CTATTGTGATCTAAAGCAGACAAAAA
*****
P_AAC97475 2881 CTATTGTGATCTAAAGCAGACAAAAA
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>2 P\_AAF44261 Human PRO331 nucleotide sequence SEQ ID NO:500. (2906 bp) [1 seg]  
Score = 2906 (5761 bits), Expect = 0.0  
Identities = 2906/2906 (100%), at 1,1-2906,2906, Strand +/-

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DNA40981 1 GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTTTGGTGGTGGCTGTTGGG
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P_AAF44261 1 GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTTTGGTGGTGGCTGTTGGG
DNA40981 61 TGCCTTGCAAAATGAAGGATGCAGGACGCAGCTTCTCCTGGAACCGAACGCAATGGAT
*****
P_AAF44261 61 TGCCTTGCAAAATGAAGGATGCAGGACGCAGCTTCTCCTGGAACCGAACGCAATGGAT
DNA40981 121 AAAC TGATTGTGCAAGAGAGAAGGAAGAACGAGCTTTCTTGAGGCCCTGGATCTTA
*****
P_AAF44261 121 AAAC TGATTGTGCAAGAGAGAAGGAAGAACGAGCTTTCTTGAGGCCCTGGATCTTA
DNA40981 181 ACACAAATGTGTATATGTGCACACAGGGAGCATTCAAGAACGAAATAAACCAGAGTTAGA
*****
P_AAF44261 181 ACACAAATGTGTATATGTGCACACAGGGAGCATTCAAGAACGAAATAAACCAGAGTTAGA
DNA40981 241 CCCGCGGGGTTGGTGTGTTCTGACATAAATAATCTTAAAGCAGCTGTTCCCTCC
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P_AAF44261 241 CCCGCGGGGTTGGTGTGTTCTGACATAAATAATCTTAAAGCAGCTGTTCCCTCC
DNA40981 301 CCACCCCCAAAAAAAGGATGATTGGAAATGAAGAACCGAGGATTCAAAAGAAAAAGT
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P_AAF44261 301 CCACCCCCAAAAAAAGGATGATTGGAAATGAAGAACCGAGGATTCAAAAGAAAAAGT
DNA40981 361 ATGTTCATTTCTCTATAAAGGAGAAAGTGAGCCAAGGAGATATTTGGAATGAAAG
*****
P_AAF44261 361 ATGTTCATTTCTCTATAAAGGAGAAAGTGAGCCAAGGAGATATTTGGAATGAAAG
DNA40981 421 TTTGGGGCTTTTAGTAAAGTAAAGAACCTGGTGTGGTGGTGTGTTCCCTTCTTTGAA
*****
P_AAF44261 421 TTTGGGGCTTTTAGTAAAGTAAAGAACCTGGTGTGGTGGTGTGTTCCCTTCTTTGAA
DNA40981 481 TTTCCCACAAGAGGAGAGGAAATTAAATAACATCTGCAAAGAAATTTCAGAGAAGAAA
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P\_AAF44261 481 TTTCCCACAAGAGGAGAGGAATTAAATAATACATCTGCAAAGAAATTCAAGAGAAGAAAA  
 DNA40981 541 GTTGACCGCGGCAGATTGAGGCATTGATTGGGGAGAGAAACCAGCAGAGCACAGTGG  
 P\_AAF44261 541 GTTGACCGCGGCAGATTGAGGCATTGATTGGGGAGAGAAACCAGCAGAGCACAGTGG  
 DNA40981 601 TTGTGCCTATGTTGACTAAAATTGACGGATAATTGAGCTTGGATTTCTTCATCAACC  
 P\_AAF44261 601 TTGTGCCTATGTTGACTAAAATTGACGGATAATTGAGCTTGGATTTCTTCATCAACC  
 DNA40981 661 TCCTTTTTAAATTTTATTCCCTTTGGTATCAAGATCATGCGTTCTCTGTTCTT  
 P\_AAF44261 661 TCCTTTTTAAATTTTATTCCCTTTGGTATCAAGATCATGCGTTCTCTGTTCTT  
 DNA40981 721 AACCACCTGGATTTCCATCTGGATGTTGCTGTGATCAGTCTGAAATACAACACTGTTGAAT  
 P\_AAF44261 721 AACCACCTGGATTTCCATCTGGATGTTGCTGTGATCAGTCTGAAATACAACACTGTTGAAT  
 DNA40981 781 TCCAGAAGGACCAACACCAGATAAAATTATGAATGTTGAACAAGATGACCTTACATCCACA  
 P\_AAF44261 781 TCCAGAAGGACCAACACCAGATAAAATTATGAATGTTGAACAAGATGACCTTACATCCACA  
 DNA40981 841 GCAGATAATGATAGGCCTAGGTTAACAGGGCCCTATTGACCCCCCTGCTTGTTGCT  
 P\_AAF44261 841 GCAGATAATGATAGGCCTAGGTTAACAGGGCCCTATTGACCCCCCTGCTTGTTGCT  
 DNA40981 901 GCTGGCTTCAACTTCTGTGGCTGGCTGGTCTGGTGCAGACCTGCCCTCTGT  
 P\_AAF44261 901 GCTGGCTTCAACTTCTGTGGCTGGCTGGTCTGGTGCAGACCTGCCCTCTGT  
 DNA40981 961 GTGCTCCTGCAGCAACCAGTTCAGCAAGGTGATTGTGTTCGGAAAAACCTGCGTGAGGT  
 P\_AAF44261 961 GTGCTCCTGCAGCAACCAGTTCAGCAAGGTGATTGTGTTCGGAAAAACCTGCGTGAGGT  
 DNA40981 1021 TCCGGATGGCATCTCCACCAACACACGGCTGCTGAACCTCCATGAGAACCAAATCCAGAT  
 P\_AAF44261 1021 TCCGGATGGCATCTCCACCAACACACGGCTGCTGAACCTCCATGAGAACCAAATCCAGAT  
 DNA40981 1081 CATCAAAGTGAACAGCTTCAAGCAGTTGAGGCACTTGAAATCCTACAGTTGAGTAGGAA  
 P\_AAF44261 1081 CATCAAAGTGAACAGCTTCAAGCAGTTGAGGCACTTGAAATCCTACAGTTGAGTAGGAA  
 DNA40981 1141 CCATATCAGAACCAATTGAAATTGGGGCTTCAATGGCTGGCGAACCTCAACACTCTGGA  
 P\_AAF44261 1141 CCATATCAGAACCAATTGAAATTGGGGCTTCAATGGCTGGCGAACCTCAACACTCTGGA  
 DNA40981 1201 ACTCTTGACAATCGTCTTACCATCCCAGTGGAGCTTTGTATACTGTCTAAACT  
 P\_AAF44261 1201 ACTCTTGACAATCGTCTTACCATCCCAGTGGAGCTTTGTATACTGTCTAAACT  
 DNA40981 1261 GAAGGAGCTCTGGTGCAGAACACACCCATTGAAAGCATCCCTTATGCTTTAACAG  
 P\_AAF44261 1261 GAAGGAGCTCTGGTGCAGAACACACCCATTGAAAGCATCCCTTATGCTTTAACAG  
 DNA40981 1321 AATTCCCTCTTGCGCCGACTAGACTTAGGGAAATTGAAAAGACTTCATACATCTCAGA  
 P\_AAF44261 1321 AATTCCCTCTTGCGCCGACTAGACTTAGGGAAATTGAAAAGACTTCATACATCTCAGA  
 DNA40981 1381 AGGTGCCTTGAAGGTCTGTCCAACCTGAGGTATTGAAACCTTGCCATGTGCAACCTCG  
 P\_AAF44261 1381 AGGTGCCTTGAAGGTCTGTCCAACCTGAGGTATTGAAACCTTGCCATGTGCAACCTCG  
 DNA40981 1441 GGAAATCCCTAACCTCACACCGCTCATAAAACCTAGATGAGCTGGATTTCTGGGAATCA

BLAST RESULTS A-19

P_AAF44261	1441	*****GGAAATCCCTAACCTCACACCGCTCATAAAAGTAGATGAGCTGGATCTTCTGGGAATCA
DNA40981	1501	*****TTTATCTGCCATCAGGCCTGGCTCTTCAGGGTTGATGCACCTCAAAAAGTGTGGAT
P_AAF44261	1501	*****TTTATCTGCCATCAGGCCTGGCTCTTCAGGGTTGATGCACCTCAAAAAGTGTGGAT
DNA40981	1561	*****GATACAGTCCCAGATTCAAGTGATTGAACCGAATGCCTTGACAACCTCAGTCACTAGT
P_AAF44261	1561	*****GATACAGTCCCAGATTCAAGTGATTGAACCGAATGCCTTGACAACCTCAGTCACTAGT
DNA40981	1621	*****GGAGATCAACCTGGCACACAATAATCTAACATTACTGCCTCATGACCTTCACTCCCT
P_AAF44261	1621	*****GGAGATCAACCTGGCACACAATAATCTAACATTACTGCCTCATGACCTTCACTCCCT
DNA40981	1681	*****GCATCATCTAGAGCGGATACATTACATCACAAACCTTGGAACTGTAAGTGTGACATACT
P_AAF44261	1681	*****GCATCATCTAGAGCGGATACATTACATCACAAACCTTGGAACTGTAAGTGTGACATACT
DNA40981	1741	*****GTGGCTCAGCTGGTGGATAAAAGACATGGCCCCCTCGAACACAGCTGTTGTGCCGGTG
P_AAF44261	1741	*****GTGGCTCAGCTGGTGGATAAAAGACATGGCCCCCTCGAACACAGCTGTTGTGCCGGTG
DNA40981	1801	*****TAACACTCCTCCCAATCTAAAGGGGAGGTACATTGGAGAGCTCGACCAGAATTACTTCAC
P_AAF44261	1801	*****TAACACTCCTCCCAATCTAAAGGGGAGGTACATTGGAGAGCTCGACCAGAATTACTTCAC
DNA40981	1861	*****ATGCTATGCTCCGGTGATTGTGGAGCCCCCTGCAGACCTCAATGTCAGTGAAAGGCATGGC
P_AAF44261	1861	*****ATGCTATGCTCCGGTGATTGTGGAGCCCCCTGCAGACCTCAATGTCAGTGAAAGGCATGGC
DNA40981	1921	*****AGCTGAGCTGAAATGTCGGGCTCCACATCCCTGACATCTGTATCTGGATTACTCCAAA
P_AAF44261	1921	*****AGCTGAGCTGAAATGTCGGGCTCCACATCCCTGACATCTGTATCTGGATTACTCCAAA
DNA40981	1981	*****TGGAACAGTCATGACACATGGGGCGTACAAAGTGCAGGATAGCTGTGCTCAGTGATGGTAC
P_AAF44261	1981	*****TGGAACAGTCATGACACATGGGGCGTACAAAGTGCAGGATAGCTGTGCTCAGTGATGGTAC
DNA40981	2041	*****GTTAAATTCACAAATGTAAGTGCAGAATCAGGCATGTACACATGTATGGTGAGTAA
P_AAF44261	2041	*****GTTAAATTCACAAATGTAAGTGCAGAATCAGGCATGTACACATGTATGGTGAGTAA
DNA40981	2101	*****TTCCGTTGGAAATACTACTGCTTCAGCCACCCCTGAATGTTACTGCAGCAACCAACTACTCC
P_AAF44261	2101	*****TTCCGTTGGAAATACTACTGCTTCAGCCACCCCTGAATGTTACTGCAGCAACCAACTACTCC
DNA40981	2161	*****TTTCTTACTTTCAACCGTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGCACG
P_AAF44261	2161	*****TTTCTTACTTTCAACCGTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGCACG
DNA40981	2221	*****GACCACAGATAACAATGTGGTCCCCTCCAGTGACTGGGAGACCAATGTGAC
P_AAF44261	2221	*****GACCACAGATAACAATGTGGTCCCCTCCAGTGACTGGGAGACCAATGTGAC
DNA40981	2281	*****CACCTCTCTCACACCCACAGAGCACAAGGTCGACAGAGAAAACCTTCACCATCCCAGTGAC
P_AAF44261	2281	*****CACCTCTCTCACACCCACAGAGCACAAGGTCGACAGAGAAAACCTTCACCATCCCAGTGAC
DNA40981	2341	*****TGATATAAACAGTGGGATCCCAGGAATTGATGAGGTGATGAAGACTACCAAAATCATCAT
P_AAF44261	2341	*****TGATATAAACAGTGGGATCCCAGGAATTGATGAGGTGATGAAGACTACCAAAATCATCAT
DNA40981	2401	*****TGGGTGTTTGTGGCCATCACACTCATGGCTGCAGTGATGCTGGTCATTTCTACAAGAT

P\_AAF44261 2401 TGGGTGTTTGTGCCATCACACTCATGGCTGCAGTGA  
 DNA40981 2461 GAGGAAGCAGCACCATCGCAAACCATCACGCCCAACAA  
 P\_AAF44261 2461 GAGGAAGCAGCACCATCGCAAACCATCACGCCCAACAA  
 DNA40981 2521 TGTGGATGATGAGATTACGGGAGACACCCATGGAAAGCCACCTG  
 P\_AAF44261 2521 TGTGGATGATGAGATTACGGGAGACACCCATGGAAAGCCACCTG  
 DNA40981 2581 CGAGCATGAGCACCTAACTACTATAACTCATACAATCTCCCTAAC  
 P\_AAF44261 2581 CGAGCATGAGCACCTAACTACTATAACTCATACAATCTCCCTAAC  
 DNA40981 2641 AGTTAACACAATAATTCAATAACACAGTCAGTCAGTGATGAACCG  
 P\_AAF44261 2641 AGTTAACACAATAATTCAATAACACAGTCAGTCAGTGATGAACCG  
 DNA40981 2701 CTCTAAAGACAATGTACAAGAGACTCAAATCTAAACATTACAGT  
 P\_AAF44261 2701 CTCTAAAGACAATGTACAAGAGACTCAAATCTAAACATTACAGT  
 DNA40981 2761 ACAATCAAAAAAAAGACAGTTTACAAAAAATGACACAAATGACTGG  
 P\_AAF44261 2761 ACAATCAAAAAAAAGACAGTTTACAAAAAATGACACAAATGACTGG  
 DNA40981 2821 TTTCAAAAAGTGTCTTACAAAAAATGACACAAATGACTGGCTAAATCT  
 P\_AAF44261 2821 TTTCAAAAAGTGTCTTACAAAAAATGACACAAATGACTGGCTAAATCT  
 P\_AAF44261 2881 CTATTGTGATCTAAAGCAGACAAAA  
 DNA40981 2881 CTATTGTGATCTAAAGCAGACAAAA  
 P\_AAF44261 2881 CTATTGTGATCTAAAGCAGACAAAA  
 >3 P\_AAF72423 Human PRO331 cDNA, Expect = 0.0 [1 seg]  
 Score = 2906 (5761 bits), Expect = 0.0  
 Identities = 2906/2906 (100%), at 1,1-2906,2906, Strand +/  
 DNA40981 1 GGGGAGAGGAATTGACCATGTAAAGGAGACTTTTTGGTGGTGGCTGGGG  
 P\_AAF72423 1 GGGGAGAGGAATTGACCATGTAAAGGAGACTTTTTGGTGGTGGCTGGGG  
 DNA40981 61 TGCCTGAAAAATGAAGGATGCAGGACGCTTCCTGAAACCGAACGCAATGGAT  
 P\_AAF72423 61 TGCCTGAAAAATGAAGGATGCAGGACGCTTCCTGAAACCGAACGCAATGGAT  
 DNA40981 121 AAACGTATTGTCAAGAGAGAAGGAAGAACGAAGCTTTCTGTGAGCCCTGGATCTTA  
 P\_AAF72423 121 AACTGTATTGTCAAGAGAGAAGGAAGAACGAAGCTTTCTGTGAGCCCTGGATCTTA  
 DNA40981 181 ACACAAATGTATATGTGCACACAGGGAGCTTCAAGAATGAAATAACCAGAGTTAGA  
 P\_AAF72423 181 ACACAAATGTATATGTGCACACAGGGAGCTTCAAGAATGAAATAACCAGAGTTAGA  
 DNA40981 241 CCCGGGGGGTTGGTGTGTTCTGACATAAATAATCTAAAGCAGCTGTTCCCTCC  
 P\_AAF72423 241 CCCGGGGGGTTGGTGTGTTCTGACATAAATAATCTAAAGCAGCTGTTCCCTCC  
 DNA40981 301 CCACCCCCAAAAAAAGGATGATTGAAATGAAGAACCGAGGATTCACAAAGAAAAAGT  
 P\_AAF72423 301 CCACCCCCAAAAAAAGGATGATTGAAATGAAGAACCGAGGATTCACAAAGAAAAAGT  
 DNA40981 361 ATGTTCATTTCTCTATAAGGAGAAAGTGAGCCAAGGAGATTTTGGAAATGAAAG

BLAST RESULTS A-8

P_AAF72423	361	***** ATGTCATTTCTATAAAGGAGAAAGTGAGCCAAGGAGATTTTGAATGAAAAG
DNA40981	421	***** TTTGGGGCTTTTAGTAAAGTAAGAACACTGGTGTGGTGGTTCCCTTCTTTGAA
P_AAF72423	421	***** TTTGGGGCTTTTAGTAAAGTAAGAACACTGGTGTGGTGGTTCCCTTCTTTGAA
DNA40981	481	***** TTTCCCACAAGAGGAGAGGAATTAAATAACATCTGCAAAGAAATTCAAGAGAAGAAA
P_AAF72423	481	***** TTTCCCACAAGAGGAGAGGAATTAAATAACATCTGCAAAGAAATTCAAGAGAAGAAA
DNA40981	541	***** GTTGACCGCGGCAGATTGAGGCATTGATTGGGGAGAGAAACCAGCAGAGCACAGTTGGA
P_AAF72423	541	***** GTTGACCGCGGCAGATTGAGGCATTGATTGGGGAGAGAAACCAGCAGAGCACAGTTGGA
DNA40981	601	***** TTTGTGCCTATGTTGACTAAAATTGACGGATAATTGCAGTTGGATTTCTTCAACC
P_AAF72423	601	***** TTTGTGCCTATGTTGACTAAAATTGACGGATAATTGCAGTTGGATTTCTTCAACC
DNA40981	661	***** TCCTTTTTAAATTTCATTCTGGTATCAAGATCATGCGTTCTTGTCTT
P_AAF72423	661	***** TCCTTTTTAAATTTCATTCTGGTATCAAGATCATGCGTTCTTGTCTT
DNA40981	721	***** AACCACCTGGATTCCATCTGGATGTTGCTGTGATCAGTCTGAAATACAACGTGTTGAAT
P_AAF72423	721	***** AACCACCTGGATTCCATCTGGATGTTGCTGTGATCAGTCTGAAATACAACGTGTTGAAT
DNA40981	781	***** TCCAGAAGGACCAACACCAGATAAAATTATGAATGTTGAACAAGATGACCTTACATCCACA
P_AAF72423	781	***** TCCAGAAGGACCAACACCAGATAAAATTATGAATGTTGAACAAGATGACCTTACATCCACA
DNA40981	841	***** GCAGATAATGATAGGCCTAGGTTAACAGGGCCCTATTGACCCCTGCTTGTTGCT
P_AAF72423	841	***** GCAGATAATGATAGGCCTAGGTTAACAGGGCCCTATTGACCCCTGCTTGTTGCT
DNA40981	901	***** GCTGGCTCTCAACTTCTGTGGCTGGCTGGTCTGGTGCAGACCTGCCCTCTGT
P_AAF72423	901	***** GCTGGCTCTCAACTTCTGTGGCTGGCTGGTCTGGTGCAGACCTGCCCTCTGT
DNA40981	961	***** GTGCTCCTGCAGCAACCAGTTCAGCAAGGTGATTGTGTCGGAAAAACCTGCGTGAGGT
P_AAF72423	961	***** GTGCTCCTGCAGCAACCAGTTCAGCAAGGTGATTGTGTCGGAAAAACCTGCGTGAGGT
DNA40981	1021	***** TCCGGATGGCATCTCACCACACACGGCTGCTGAACCTCCATGAGAACCAAATCCAGAT
P_AAF72423	1021	***** TCCGGATGGCATCTCACCACACACGGCTGCTGAACCTCCATGAGAACCAAATCCAGAT
DNA40981	1081	***** CATCAAAGTGAACAGCTTCAAGCAGCTTGAGGCACTTGGAAATCCTACAGTTGAGTAGGAA
P_AAF72423	1081	***** CATCAAAGTGAACAGCTTCAAGCAGCTTGAGGCACTTGGAAATCCTACAGTTGAGTAGGAA
DNA40981	1141	***** CCATATCAGAACATTGAAATTGGGGCTTCAATGGTCTGGCGAACCTCAACACTCTGGA
P_AAF72423	1141	***** CCATATCAGAACATTGAAATTGGGGCTTCAATGGTCTGGCGAACCTCAACACTCTGGA
DNA40981	1201	***** ACTCTTGACAATCGTCTTACTACCATCCGAATGGAGCTTTGTATACTGTCTAAACT
P_AAF72423	1201	***** ACTCTTGACAATCGTCTTACTACCATCCGAATGGAGCTTTGTATACTGTCTAAACT
DNA40981	1261	***** GAAGGAGCTCTGGTGCAGAACACCCCCATTGAAAGCATCCCTTATGCTTTAACAG
P_AAF72423	1261	***** GAAGGAGCTCTGGTGCAGAACACCCCCATTGAAAGCATCCCTTATGCTTTAACAG
DNA40981	1321	AATTCTCTTGCAGCGACTAGACTTAGGGATTGAAAAGACTTCATACATCTCAGA

\*\*\*\*\*  
P\_AAF72423 1321 AATTCCCTTCTTGCGCCGACTAGACTTAGGGG  
DNA40981 1381 AGGTGCCTTGAAGGTCTGTCCAACTTGAGGTATTT  
\*\*\*\*\*  
P\_AAF72423 1381 AGGTGCCTTGAAGGTCTGTCCAACTTGAGGTATTTGAACATCTCAGA  
DNA40981 1441 GGAAATCCCTAACCTCACACCGCTCATAAAACATAGATGAGCTGGACACCTTCG  
\*\*\*\*\*  
P\_AAF72423 1441 GGAAATCCCTAACCTCACACCGCTCATAAAACATAGATGAGCTGGATCTTCG  
DNA40981 1501 TTTATCTGCCATCAGGCCTGGCTCTTCCAGGGTTGATGCACCTCAAAAAA\*\*  
\*\*\*\*\*  
P\_AAF72423 1501 TTTATCTGCCATCAGGCCTGGCTCTTCCAGGGTTGATGCACCTCAAAAACGT  
DNA40981 1561 GATACAGTCCCAGATTCAAGTGATTGAACGGAATGCCTTGACAACCTCAGTCAGTCAGTAGT  
\*\*\*\*\*  
P\_AAF72423 1561 GATACAGTCCCAGATTCAAGTGATTGAACGGAATGCCTTGACAACCTCAGTCAGTCAGTAGT  
DNA40981 1621 GGAGATCAACCTGGCACACAATAATCTAACATTACTGCCTCATGACCTTCACTCCCTT  
\*\*\*\*\*  
P\_AAF72423 1621 GGAGATCAACCTGGCACACAATAATCTAACATTACTGCCTCATGACCTTCACTCCCTT  
DNA40981 1681 GCATCATCTAGAGCGGATACATTACATCACAAACCCCTGGAACGTAACTGTGACATACT  
\*\*\*\*\*  
P\_AAF72423 1681 GCATCATCTAGAGCGGATACATTACATCACAAACCCCTGGAACGTAACTGTGACATACT  
DNA40981 1741 GTGGCTCAGCTGGGGATAAAAGACATGGCCCCCTCGAACACAGCTTGTGCCCCGGTG  
\*\*\*\*\*  
P\_AAF72423 1741 GTGGCTCAGCTGGGGATAAAAGACATGGCCCCCTCGAACACAGCTTGTGCCCCGGTG  
DNA40981 1801 TAACACTCCTCCAACTAAAGGGGAGGTACATTGGAGAGCTGACCAGAAATTACTTCAC  
\*\*\*\*\*  
P\_AAF72423 1801 TAACACTCCTCCAACTAAAGGGGAGGTACATTGGAGAGCTGACCAGAAATTACTTCAC  
DNA40981 1861 ATGCTATGCTCCGGTGATTGGAGCCCCCTGCAGACACTCAATGTCACTGAAGGCATGGC  
\*\*\*\*\*  
P\_AAF72423 1861 ATGCTATGCTCCGGTGATTGGAGCCCCCTGCAGACACTCAATGTCACTGAAGGCATGGC  
DNA40981 1921 AGCTGAGCTGAAATGCGGGCCTCCACATCCCTGACATCTGTATCTGGATTACTCCAA  
\*\*\*\*\*  
P\_AAF72423 1921 AGCTGAGCTGAAATGCGGGCCTCCACATCCCTGACATCTGTATCTGGATTACTCCAA  
DNA40981 1981 TGGAACAGTCATGACACATGGGGCGTACAAAGTGCAGGATAGCTGTGCTCAGTGTGATGGTAC  
\*\*\*\*\*  
P\_AAF72423 1981 TGGAACAGTCATGACACATGGGGCGTACAAAGTGCAGGATAGCTGTGCTCAGTGTGATGGTAC  
DNA40981 2041 GTTAAATTCACAAATGTAACGTGCAAGATAAGGCATGTACACATGTATGGTGAGTAA  
\*\*\*\*\*  
P\_AAF72423 2041 GTTAAATTCACAAATGTAACGTGCAAGATAAGGCATGTACACATGTATGGTGAGTAA  
DNA40981 2101 TTCCGTTGGGAATACTACTGCTTCAGCCACCTGAATGTTACTGCAGCAACCAACTACTCC  
\*\*\*\*\*  
P\_AAF72423 2101 TTCCGTTGGGAATACTACTGCTTCAGCCACCTGAATGTTACTGCAGCAACCAACTACTCC  
DNA40981 2161 TTTCTCTTACTTTCAACCGTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGCACG  
\*\*\*\*\*  
P\_AAF72423 2161 TTTCTCTTACTTTCAACCGTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGCACG  
DNA40981 2221 GACCACAGATAACAAATGCGGGCCTCCACTCCAGTGGTCAGTGGAGACCACCAATGTGAC  
\*\*\*\*\*  
P\_AAF72423 2221 GACCACAGATAACAAATGCGGGCCTCCACTCCAGTGGTCAGTGGAGACCACCAATGTGAC  
DNA40981 2281 CACCTCTCACACCACAGAGCACAAGGTCGACAGAGAAAACCTCACCATCCCAGTGAC

P\_AAF72423 2281 \*\*\*\*CACCTCTCACACCACAGAGCACAAGGTC  
 DNA40981 2341 TGATATAAACAGTGGATCCCAGGAATTGATGAGG  
 P\_AAF72423 2341 TGATATAAACAGTGGATCCCAGGAATTGATGAGGTCAATCCAGTGAC  
 DNA40981 2401 TGGGTGTTGTGCCATCACACTCATGGCTGCAGTGATGCTGATCATCAT  
 P\_AAF72423 2401 TGGGTGTTGTGCCATCACACTCATGGCTGCAGTGATGCTGGTCATCAT  
 DNA40981 2461 GAGGAAGCAGCACCATCGCAAAACCATCACGCCCAACAAGGACTGTTGAA  
 P\_AAF72423 2461 GAGGAAGCAGCACCATCGCAAAACCATCACGCCCAACAAGGACTGTTGAAATTAGAT  
 DNA40981 2521 TGTGGATGATGAGATTACGGGAGACACACCCATGGAAAGCCACCTGCCATGCCTGCTAT  
 P\_AAF72423 2521 TGTGGATGATGAGATTACGGGAGACACACCCATGGAAAGCCACCTGCCATGCCTGCTAT  
 DNA40981 2581 CGAGCATGAGCACCTAAATCACTATAACTCATACAAATCTCCCTCAACCACACAAC  
 P\_AAF72423 2581 CGAGCATGAGCACCTAAATCACTATAACTCATACAAATCTCCCTCAACCACACAAC  
 DNA40981 2641 AGTTAACACAATAATTCAATACACAGTTCACTGCATGAACCGTTATTGATCCGAATGAA  
 P\_AAF72423 2641 AGTTAACACAATAATTCAATACACAGTTCACTGCATGAACCGTTATTGATCCGAATGAA  
 DNA40981 2701 CTCTAAAGACAATGTACAAGAGACTCAAATCTAAAACATTACAGAGTTACAAAAACAA  
 P\_AAF72423 2701 CTCTAAAGACAATGTACAAGAGACTCAAATCTAAAACATTACAGAGTTACAAAAACAA  
 DNA40981 2761 ACAATCAAAAAAAAGACAGTTATTAAAATGACACAAATGACTGGCTAAATCTACTG  
 P\_AAF72423 2761 ACAATCAAAAAAAAGACAGTTATTAAAATGACACAAATGACTGGCTAAATCTACTG  
 DNA40981 2821 TTTCAAAAAGTGTCTTACAAAAAAACAAAAAGAAAAGAAATTATTATTAAAAATT  
 P\_AAF72423 2821 TTTCAAAAAGTGTCTTACAAAAAAACAAAAAGAAAAGAAATTATTATTAAAAATT  
 DNA40981 2881 CTATTGTGATCTAACGAGACAAAAA  
 P\_AAF72423 2881 CTATTGTGATCTAACGAGACAAAAA

>4 P\_AAZ52207 Human PRO331 protein encoding cDNA, UNQ292. DNA, PAT 18-JUL-2000  
 (2906 bp) [1 seg]

Score = 2906 (5761 bits), Expect = 0.0

Identities = 2906/2906 (100%), at 1,1-2906,2906, Strand +/-

DNA40981 1 GGGGAGAGGAATTGACCATGTAAAGGAGACTTTTTTTGGTGGTGGCTGTTGGG  
 P\_AAZ52207 1 GGGGAGAGGAATTGACCATGTAAAGGAGACTTTTTTTGGTGGTGGCTGTTGGG  
 DNA40981 61 TGCCTTGCAAAATGAAGGATGCAGGACGCAGCTTCTCCTGGAACCGAACGCAATGGAT  
 P\_AAZ52207 61 TGCCTTGCAAAATGAAGGATGCAGGACGCAGCTTCTCCTGGAACCGAACGCAATGGAT  
 DNA40981 121 AAACTGATTGTGCAAGAGAGAAGGAAGAACGAGCTTTCTGTGAGCCCTGGATCTTA  
 P\_AAZ52207 121 AAACTGATTGTGCAAGAGAGAAGGAAGAACGAGCTTTCTGTGAGCCCTGGATCTTA  
 DNA40981 181 ACACAAATGTGTATATGTGCACACAGGGAGCATTCAAGAACGAAATGAAATAACCAGAGTTAGA  
 P\_AAZ52207 181 ACACAAATGTGTATATGTGCACACAGGGAGCATTCAAGAACGAAATGAAATAACCAGAGTTAGA

DNA40981 241 CCCGCGGGGTTGGTGTGTTCTGACATAAATAAA  
 P\_AAZ52207 241 CCCGCGGGGTTGGTGTGTTCTGACATAAATAAA  
 DNA40981 301 CCACCCCCAAAAAAAGGATGATTGAAATGAAGAACCGAGGGTTCCCTCC  
 P\_AAZ52207 301 CCACCCCCAAAAAAAGGATGATTGAAATGAAGAACCGAGGATTCCTCC  
 DNA40981 361 ATGTTCATTTCTCTATAAAGGAGAAAGTGAGCCAAGGAGATATTTT  
 P\_AAZ52207 361 ATGTTCATTTCTCTATAAAGGAGAAAGTGAGCCAAGGAGATATTTTGGAA  
 DNA40981 421 TTTGGGGCTTTTAGTAAAGTAAGAACTGGTGTGGTGGTGTTCCTTCTTT  
 P\_AAZ52207 421 TTTGGGGCTTTTAGTAAAGTAAGAACTGGTGTGGTGGTGTTCCTTCTTTGA  
 DNA40981 481 TTTCCCACAAGAGGAGAGGAAATTAAATAATACATCTGAAAGAAATTCAAGAGAAGAAA  
 P\_AAZ52207 481 TTTCCCACAAGAGGAGAGGAAATTAAATAATACATCTGAAAGAAATTCAAGAGAAGAAA  
 DNA40981 541 GTTGACCGCGGCAGATTGAGGCATTGATTGGGGAGAGAACAGCAGAGCACAGTTGGA  
 P\_AAZ52207 541 GTTGACCGCGGCAGATTGAGGCATTGATTGGGGAGAGAACAGCAGAGCACAGTTGGA  
 DNA40981 601 TTTGTGCCTATGTTGACTAAATTGACGGATAATTGCAGTTGGATTTCTTCATCAACC  
 P\_AAZ52207 601 TTTGTGCCTATGTTGACTAAATTGACGGATAATTGCAGTTGGATTTCTTCATCAACC  
 DNA40981 661 TCCTTTTTAAATTTTATTCTTTGGTATCAAGATCATGCGTTTCTCTTGTCT  
 P\_AAZ52207 661 TCCTTTTTAAATTTTATTCTTTGGTATCAAGATCATGCGTTTCTCTTGTCT  
 DNA40981 721 AACCACCTGGATTCATCTGGATGTTGCTGTGATCAGTCTGAAATACAACGTGGAT  
 P\_AAZ52207 721 AACCACCTGGATTCATCTGGATGTTGCTGTGATCAGTCTGAAATACAACGTGGAT  
 DNA40981 781 TCCAGAAGGACCAACACCGATAAAATTATGAATGTTGAAACAAGATGACCTACATCCACA  
 P\_AAZ52207 781 TCCAGAAGGACCAACACCGATAAAATTATGAATGTTGAAACAAGATGACCTACATCCACA  
 DNA40981 841 GCAGATAATGATAGGTCTTAGGTTAACAGGGCCCTATTGACCCCTGCTGTGGTGGCT  
 P\_AAZ52207 841 GCAGATAATGATAGGTCTTAGGTTAACAGGGCCCTATTGACCCCTGCTGTGGTGGCT  
 DNA40981 901 GCTGGCTTCAACTTGTGGCTGGCTGGTCTGGTGGCTCAGACCTGCCCTCTGT  
 P\_AAZ52207 901 GCTGGCTTCAACTTGTGGCTGGCTGGTCTGGTGGCTCAGACCTGCCCTCTGT  
 DNA40981 961 GTGCTCCTGCAGCAACCAGTCAGCAAGGTGATTGTGTTCGGAAAAACCTGCGTGAGGT  
 P\_AAZ52207 961 GTGCTCCTGCAGCAACCAGTCAGCAAGGTGATTGTGTTCGGAAAAACCTGCGTGAGGT  
 DNA40981 1021 TCCGGATGGCATCTCCACCAACACACGGCTGCTGAACCTCCATGAGAACCAAATCCAGAT  
 P\_AAZ52207 1021 TCCGGATGGCATCTCCACCAACACACGGCTGCTGAACCTCCATGAGAACCAAATCCAGAT  
 DNA40981 1081 CATCAAAGTGAACAGCTCAAGCACTTGAGGCACCTGGAAATCCTACAGTTGAGTAGGAA  
 P\_AAZ52207 1081 CATCAAAGTGAACAGCTCAAGCACTTGAGGCACCTGGAAATCCTACAGTTGAGTAGGAA  
 DNA40981 1141 CCATATCAGAACCAATTGAAATTGGGGCTTCAATGGTCTGGCGAACCTAACACTCTGGA  
 P\_AAZ52207 1141 CCATATCAGAACCAATTGAAATTGGGGCTTCAATGGTCTGGCGAACCTAACACTCTGGA

RESULTS

BLAST RESULTS A-12

DNA40981	1201	ACTCTTGACAATCGTCTTACCTACCCTCCGAATGGAGCTTTGTATACTGTCTAACT *****
P_AAZ52207	1201	ACTCTTGACAATCGTCTTACCTACCCTCCGAATGGAGCTTTGTATACTGTCTAACT *****
DNA40981	1261	GAAGGAGCTCTGGTGCAGAACAAACCCCATTGAAAGCATTCCCTCTTATGCTTTAACAG *****
P_AAZ52207	1261	GAAGGAGCTCTGGTGCAGAACAAACCCCATTGAAAGCATTCCCTCTTATGCTTTAACAG *****
DNA40981	1321	AATTCCCTCTTGCGCCGACTAGACTTAGGGGAATTGAAAAGACTTTCATACATCTCAGA *****
P_AAZ52207	1321	AATTCCCTCTTGCGCCGACTAGACTTAGGGGAATTGAAAAGACTTTCATACATCTCAGA *****
DNA40981	1381	AGGTGCCTTGAAGGTCTGTCCAACCTGAGGTATTGAACCTGCCATGTGCAACCTTCG *****
P_AAZ52207	1381	AGGTGCCTTGAAGGTCTGTCCAACCTGAGGTATTGAACCTGCCATGTGCAACCTTCG *****
DNA40981	1441	GGAAATCCCTAACCTCACACCGCTCATAAAAGTAGATGAGCTGGATCTTCTGGGAATCA *****
P_AAZ52207	1441	GGAAATCCCTAACCTCACACCGCTCATAAAAGTAGATGAGCTGGATCTTCTGGGAATCA *****
DNA40981	1501	TTTATCTGCCATCAGGCCTGGCTTTCCAGGGTTGATGCACCTTCACAAACTGTGGAT *****
P_AAZ52207	1501	TTTATCTGCCATCAGGCCTGGCTTTCCAGGGTTGATGCACCTTCACAAACTGTGGAT *****
DNA40981	1561	GATACAGTCCCAGATTCAAGTGATTGAACCGGAATGCCCTTGACAAACCTTCAGTCAGTAGT *****
P_AAZ52207	1561	GATACAGTCCCAGATTCAAGTGATTGAACCGGAATGCCCTTGACAAACCTTCAGTCAGTAGT *****
DNA40981	1621	GGAGATCAACCTGGCACACAATAATCTAACATTACTGCCTCATGACCTCTTCACCCCTT *****
P_AAZ52207	1621	GGAGATCAACCTGGCACACAATAATCTAACATTACTGCCTCATGACCTCTTCACCCCTT *****
DNA40981	1681	GCATCATCTAGAGCGGATACATTACATCACAAACCTTGGAACTGTAACGTGACATACT *****
P_AAZ52207	1681	GCATCATCTAGAGCGGATACATTACATCACAAACCTTGGAACTGTAACGTGACATACT *****
DNA40981	1741	GTGGCTCAGCTGGGGATAAAAGACATGGCCCCCTCGAACACAGCTTGTGCCCCGGTG *****
P_AAZ52207	1741	GTGGCTCAGCTGGGGATAAAAGACATGGCCCCCTCGAACACAGCTTGTGCCCCGGTG *****
DNA40981	1801	TAACACTCCTCCCAATCTAAAGGGGAGGTACATTGGAGAGCTCGACCAGAATTACTTCAC *****
P_AAZ52207	1801	TAACACTCCTCCCAATCTAAAGGGGAGGTACATTGGAGAGCTCGACCAGAATTACTTCAC *****
DNA40981	1861	ATGCTATGCTCCGGTGATTGTGGAGCCCCCTGCAGACCTCAATGTCAGTGAAAGGCATGGC *****
P_AAZ52207	1861	ATGCTATGCTCCGGTGATTGTGGAGCCCCCTGCAGACCTCAATGTCAGTGAAAGGCATGGC *****
DNA40981	1921	AGCTGAGCTGAAATGTCGGGCCTCCACATCCCTGACATCTGTATCTTGGATTACTCCAAA *****
P_AAZ52207	1921	AGCTGAGCTGAAATGTCGGGCCTCCACATCCCTGACATCTGTATCTTGGATTACTCCAAA *****
DNA40981	1981	TGGAACAGTCATGACACATGGGGCGTACAAAGTGCAGTAGCTGTGCTCAGTGATGGTAC *****
P_AAZ52207	1981	TGGAACAGTCATGACACATGGGGCGTACAAAGTGCAGTAGCTGTGCTCAGTGATGGTAC *****
DNA40981	2041	GTTAAATTTCACAAATGTAACGTGCAAGATAACAGGCATGTACACATGTATGGTGAGTAA *****
P_AAZ52207	2041	GTTAAATTTCACAAATGTAACGTGCAAGATAACAGGCATGTACACATGTATGGTGAGTAA *****
DNA40981	2101	TTCCGTTGGGAATACTACTGCTTCAGCCACCCCTGAATGTTACTGCAGCAACCAACTACTCC *****
P_AAZ52207	2101	TTCCGTTGGGAATACTACTGCTTCAGCCACCCCTGAATGTTACTGCAGCAACCAACTACTCC *****

RESULTS A-13

BLAST

DNA40981	2161	TTTCTCTTACTTTCAACCGTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGCACG *****
P_AAZ52207	2161	TTTCTCTTACTTTCAACCGTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGCACG *****
DNA40981	2221	GACCACAGATAACAATGTGGTCCCCTCCAGTGACTGGGAGACCAATGTGAC *****
P_AAZ52207	2221	GACCACAGATAACAATGTGGTCCCCTCCAGTGACTGGGAGACCAATGTGAC *****
DNA40981	2281	CACCTCTCTCACACCACAGAGCACAAGGTCAGAGAGAAAACCTTCACCATCCCAGTGAC *****
P_AAZ52207	2281	CACCTCTCTCACACCACAGAGCACAAGGTCAGAGAGAAAACCTTCACCATCCCAGTGAC *****
DNA40981	2341	TGATATAAACAGTGGGATCCCAGGAATTGATGAGGTCAAGAGACTACCAAAATCATCAT *****
P_AAZ52207	2341	TGATATAAACAGTGGGATCCCAGGAATTGATGAGGTCAAGAGACTACCAAAATCATCAT *****
DNA40981	2401	TGGGTGTTTGTGGCCATCACACTCATGGCTGCAGTGATGCTGGTCATTTCTACAAGAT *****
P_AAZ52207	2401	TGGGTGTTTGTGGCCATCACACTCATGGCTGCAGTGATGCTGGTCATTTCTACAAGAT *****
DNA40981	2461	GAGGAAGCAGCACCATCGGAAACCATCACGCCCAACAAGGACTGTTGAAATTATTA *****
P_AAZ52207	2461	GAGGAAGCAGCACCATCGGAAACCATCACGCCCAACAAGGACTGTTGAAATTATTA *****
DNA40981	2521	TGTGGATGATGAGATTACGGGAGACACACCCATGGAAAGCCACCTGCCATGCCTGCTAT *****
P_AAZ52207	2521	TGTGGATGATGAGATTACGGGAGACACACCCATGGAAAGCCACCTGCCATGCCTGCTAT *****
DNA40981	2581	CGAGCATGAGCACCTAAATCACTATAACTCATACAAATCTCCCTCAACCACACAAC *****
P_AAZ52207	2581	CGAGCATGAGCACCTAAATCACTATAACTCATACAAATCTCCCTCAACCACACAAC *****
DNA40981	2641	AGTTAACACAATAAATTCAATACACAGTTCACTGCAGTGAACCGTTATTGATCCGAATGAA *****
P_AAZ52207	2641	AGTTAACACAATAAATTCAATACACAGTTCACTGCAGTGAACCGTTATTGATCCGAATGAA *****
DNA40981	2701	CTCTAAAGACAATGTACAAGAGACTCAAATCTAAACATTACAGAGTTACAAAAAACAA *****
P_AAZ52207	2701	CTCTAAAGACAATGTACAAGAGACTCAAATCTAAACATTACAGAGTTACAAAAAACAA *****
DNA40981	2761	ACAATCAAAAAAAAGACAGTTATTAAAAATGACACAAATGACTGGCTAAATCTACTG *****
P_AAZ52207	2761	ACAATCAAAAAAAAGACAGTTATTAAAAATGACACAAATGACTGGCTAAATCTACTG *****
DNA40981	2821	TTTCAAAAAAGTGTCTTACAAAAAAACAAAAAGAAAAGAAATTATTATTAAAAATT *****
P_AAZ52207	2821	TTTCAAAAAAGTGTCTTACAAAAAAACAAAAAGAAAAGAAATTATTATTAAAAATT *****
DNA40981	2881	CTATTGTGATCTAACAGCAGACAAAAA *****
P_AAZ52207	2881	CTATTGTGATCTAACAGCAGACAAAAA

>5 P\_AAA77596 Human PRO331 cDNA sequence SEQ ID NO:106. DNA, PAT 07-NOV-2000 (2906 bp) [1 seg]

Score = 2906 (5761 bits), Expect = 0.0

Identities = 2906/2906 (100%), at 1,1-2906,2906, Strand +/-

DNA40981	1	GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTGGTGGTGGCTGTTGGG *****
P_AAA77596	1	GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTGGTGGTGGCTGTTGGG *****
DNA40981	61	TGCCTTGCAAAATGAAGGATGCAGGACCGCAGCTTCTCCTGGAACCGAACGCAATGGAT *****
P_AAA77596	61	TGCCTTGCAAAATGAAGGATGCAGGACCGCAGCTTCTCCTGGAACCGAACGCAATGGAT *****

DNA40981	121	AAACTGATTGTCAAGAGAGAAGGAAGAACGAAGCTTTCTTGTGAGCCCTGGATCTTA *****
P_AAA77596	121	AAACTGATTGTCAAGAGAGAAGGAAGAACGAAGCTTTCTTGTGAGCCCTGGATCTTA *****
DNA40981	181	ACACAAATGTGTATATGTGCACACAGGGAGCATTCAAGAAATGAAATAACCAGAGTTAGA *****
P_AAA77596	181	ACACAAATGTGTATATGTGCACACAGGGAGCATTCAAGAAATGAAATAACCAGAGTTAGA *****
DNA40981	241	CCCGCGGGGGTTGGTGTGTTCTGACATAAATAATCTTAAAGCAGCTGTTCCCTCC *****
P_AAA77596	241	CCCGCGGGGGTTGGTGTGTTCTGACATAAATAATCTTAAAGCAGCTGTTCCCTCC *****
DNA40981	301	CCACCCCCAAAAAAAGGATGATTGAAATGAAGAACCGAGGATTCACAAAGAAAAAGT *****
P_AAA77596	301	CCACCCCCAAAAAAAGGATGATTGAAATGAAGAACCGAGGATTCACAAAGAAAAAGT *****
DNA40981	361	ATGTTCATTTCTCTATAAAGGAGAAAGTGAGCCAAGGAGATATTTGGAATGAAAAG *****
P_AAA77596	361	ATGTTCATTTCTCTATAAAGGAGAAAGTGAGCCAAGGAGATATTTGGAATGAAAAG *****
DNA40981	421	TTTGGGGCTTTTAGTAAAGTAAAGAACCTGGTGTGGTGGTTTCCTTCTTTGAA *****
P_AAA77596	421	TTTGGGGCTTTTAGTAAAGTAAAGAACCTGGTGTGGTGGTGGTTTCCTTCTTTGAA *****
DNA40981	481	TTTCCCACAAGAGGAGAGGAAATTAAATAACATCTGCAAAGAAATTTCAGAGAAGAAA *****
P_AAA77596	481	TTTCCCACAAGAGGAGAGGAAATTAAATAACATCTGCAAAGAAATTTCAGAGAAGAAA *****
DNA40981	541	GTTGACCGCGGCAGATTGAGGCATTGATTGGGGAGAGAACCAGCAGAGCACAGTTGGA *****
P_AAA77596	541	GTTGACCGCGGCAGATTGAGGCATTGATTGGGGAGAGAACCAGCAGAGCACAGTTGGA *****
DNA40981	601	TTTGTGCCTATGTTGACTAAATTGACGGATAATTGCAGTTGGATTTCTTCATCAACC *****
P_AAA77596	601	TTTGTGCCTATGTTGACTAAATTGACGGATAATTGCAGTTGGATTTCTTCATCAACC *****
DNA40981	661	TCCTTTTTAAATTTCATTCTTTGGTATCAAGATCATGCGTTCTTGTCTT *****
P_AAA77596	661	TCCTTTTTAAATTTCATTCTTTGGTATCAAGATCATGCGTTCTTGTCTT *****
DNA40981	721	AACCACCTGGATTTCCATCTGGATGTTGCTGTGATCAGTCTGAAATACAACACTGTTGAAT *****
P_AAA77596	721	AACCACCTGGATTTCCATCTGGATGTTGCTGTGATCAGTCTGAAATACAACACTGTTGAAT *****
DNA40981	781	TCCAGAAGGACCAACACCAGATAAATTATGAATGTTGAAACAAGATGACCTTACATCCACA *****
P_AAA77596	781	TCCAGAAGGACCAACACCAGATAAATTATGAATGTTGAAACAAGATGACCTTACATCCACA *****
DNA40981	841	GCAGATAATGATAGGCCTAGGTTAACAGGGCCCTATTGACCCCTGCTTGTGGTGC *****
P_AAA77596	841	GCAGATAATGATAGGCCTAGGTTAACAGGGCCCTATTGACCCCTGCTTGTGGTGC *****
DNA40981	901	GCTGGCTCTCAACTTCTTGTGGCTGGCTGGCTGGCTGGCTCAGACCTGCCCTCTGT *****
P_AAA77596	901	GCTGGCTCTCAACTTCTTGTGGCTGGCTGGCTGGCTGGCTCAGACCTGCCCTCTGT *****
DNA40981	961	GTGCTCCTGCAGCAACCAGTTCAGCAAGGTGATTGTGTTCGGAAAAACCTGCGTGAGGT *****
P_AAA77596	961	GTGCTCCTGCAGCAACCAGTTCAGCAAGGTGATTGTGTTCGGAAAAACCTGCGTGAGGT *****
DNA40981	1021	TCCGGATGGCATCTCCACCAACACACAGGCTGCTGAACCTCCATGAGAACCAAATCCAGAT *****
P_AAA77596	1021	TCCGGATGGCATCTCCACCAACACACAGGCTGCTGAACCTCCATGAGAACCAAATCCAGAT *****

BLAST RESULTS A15

DNA40981	1081	CATCAAAGTGAACAGCCTCAAGCAGTGGAGGACTTGAAATCCTACAGTTGAGTAGGAA *****
P_AAA77596	1081	CATCAAAGTGAACAGCCTCAAGCAGTGGAGGACTTGAAATCCTACAGTTGAGTAGGAA *****
DNA40981	1141	CCATATCAGAACCATGAAATTGGGGCTTCATGGTCTGGCAACCTAACACTCTGGA *****
P_AAA77596	1141	CCATATCAGAACCATGAAATTGGGGCTTCATGGTCTGGCAACCTAACACTCTGGA *****
DNA40981	1201	ACTCTTGACAATCGTCTTACCATCCCAGGAGCTTTGTATACTGTCTAAACT *****
P_AAA77596	1201	ACTCTTGACAATCGTCTTACCATCCCAGGAGCTTTGTATACTGTCTAAACT *****
DNA40981	1261	GAAGGAGCTCTGGTGCAGAACACACCCCCATTGAAAGCATTGCTTATGCTTTAACAG *****
P_AAA77596	1261	GAAGGAGCTCTGGTGCAGAACACACCCCCATTGAAAGCATTGCTTATGCTTTAACAG *****
DNA40981	1321	AATTCCCTCTTGCGCCGACTAGACTTAGGGATTGAAAAGACTTACATCTCAGA *****
P_AAA77596	1321	AATTCCCTCTTGCGCCGACTAGACTTAGGGATTGAAAAGACTTACATCTCAGA *****
DNA40981	1381	AGGTGCCTTGAGGTCTGTCCAACCTGAGGTATTGAAACCTGCCATGTGCAACCTCG *****
P_AAA77596	1381	AGGTGCCTTGAGGTCTGTCCAACCTGAGGTATTGAAACCTGCCATGTGCAACCTCG *****
DNA40981	1441	GGAAATCCCTAACCTCACACCGCTCATAAAAGTAGATGAGCTGGATTTCTGGAAATCA *****
P_AAA77596	1441	GGAAATCCCTAACCTCACACCGCTCATAAAAGTAGATGAGCTGGATTTCTGGAAATCA *****
DNA40981	1501	TTTATCTGCCATCAGGCCTGGCTTTCCAGGGTTGATGCACCTTCAAAACTGTGGAT *****
P_AAA77596	1501	TTTATCTGCCATCAGGCCTGGCTTTCCAGGGTTGATGCACCTTCAAAACTGTGGAT *****
DNA40981	1561	GATACAGTCCCAGATTCAAGTGATTGAAACGGAATGCCCTGACAACCTTCAGTCAGTAGT *****
P_AAA77596	1561	GATACAGTCCCAGATTCAAGTGATTGAAACGGAATGCCCTGACAACCTTCAGTCAGTAGT *****
DNA40981	1621	GGAGATCAACCTGGCACACAATAATCTAACATTACTGCCTCATGACCTTCACTCCCT *****
P_AAA77596	1621	GGAGATCAACCTGGCACACAATAATCTAACATTACTGCCTCATGACCTTCACTCCCT *****
DNA40981	1681	GCATCATCTAGAGCGGATACATTACATCACACCCCTGGAACTGTAACTGTGACATACT *****
P_AAA77596	1681	GCATCATCTAGAGCGGATACATTACATCACACCCCTGGAACTGTAACTGTGACATACT *****
DNA40981	1741	GTGGCTCAGCTGGGGATAAAAGACATGGCCCCCTCGAACACAGCTTGTGCCCCGGTG *****
P_AAA77596	1741	GTGGCTCAGCTGGGGATAAAAGACATGGCCCCCTCGAACACAGCTTGTGCCCCGGTG *****
DNA40981	1801	TAACACTCCTCCAACTAAAGGGGAGGTACATTGGAGAGCTCGACCAGAATTACTTCAC *****
P_AAA77596	1801	TAACACTCCTCCAACTAAAGGGGAGGTACATTGGAGAGCTCGACCAGAATTACTTCAC *****
DNA40981	1861	ATGCTATGCTCCGGTGATTGTGGAGCCCCCTGCAGACCTCAATGTCAGTGAAAGGCATGGC *****
P_AAA77596	1861	ATGCTATGCTCCGGTGATTGTGGAGCCCCCTGCAGACCTCAATGTCAGTGAAAGGCATGGC *****
DNA40981	1921	AGCTGAGCTGAAATGTCGGGCCTCCACATCCCTGACATCTGTATCTGGATTACTCCAAA *****
P_AAA77596	1921	AGCTGAGCTGAAATGTCGGGCCTCCACATCCCTGACATCTGTATCTGGATTACTCCAAA *****
DNA40981	1981	TGGAACAGTCATGACACATGGGGCGTACAAAGTGCAGTAGCTGTGCTCAGTGATGGTAC *****
P_AAA77596	1981	TGGAACAGTCATGACACATGGGGCGTACAAAGTGCAGTAGCTGTGCTCAGTGATGGTAC *****

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BLAST RESULTS A10

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DNA40981	2041	GTTAAATTCACAAATGTAAGTCACTGTCAAGATAACAGGCATGTACACATGTATGGTGAGTAA *****
P_AAA77596	2041	GTTAAATTCACAAATGTAAGTCACTGTCAAGATAACAGGCATGTACACATGTATGGTGAGTAA *****
DNA40981	2101	TTCCGTTGGAAATACTACTGCTTCAGCCACCCGAATGTTACTGCAGCAACCCTACTCC *****
P_AAA77596	2101	TTCCGTTGGAAATACTACTGCTTCAGCCACCCGAATGTTACTGCAGCAACCCTACTCC *****
DNA40981	2161	TTTCTCTTACCAACCGTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGCACG *****
P_AAA77596	2161	TTTCTCTTACCAACCGTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGCACG *****
DNA40981	2221	GACCACAGATAACAATGTGGGTCCCCTCCAGTGGTCAGTGGAGACCACCAATGTGAC *****
P_AAA77596	2221	GACCACAGATAACAATGTGGGTCCCCTCCAGTGGTCAGTGGAGACCACCAATGTGAC *****
DNA40981	2281	CACCTCTCTCACACACCACAGAGCACAAGGTCGACAGAGAAAACCTTCACCATCCCAGTGAC *****
P_AAA77596	2281	CACCTCTCTCACACACCACAGAGCACAAGGTCGACAGAGAAAACCTTCACCATCCCAGTGAC *****
DNA40981	2341	TGATATAAACAGTGGGATCCCAGGAATTGATGAGGTCAAGAGACTACCAAAATCATCAT *****
P_AAA77596	2341	TGATATAAACAGTGGGATCCCAGGAATTGATGAGGTCAAGAGACTACCAAAATCATCAT *****
DNA40981	2401	TGGGTGTTTGTGGCCATCACACTCATGGCTGCAGTGATGCTGGCATTTCTACAAGAT *****
P_AAA77596	2401	TGGGTGTTTGTGGCCATCACACTCATGGCTGCAGTGATGCTGGCATTTCTACAAGAT *****
DNA40981	2461	GAGGAAGCAGCACCATCGCAAACCATCACGCCCAACAAGGACTGTTGAAATTATTA *****
P_AAA77596	2461	GAGGAAGCAGCACCATCGCAAACCATCACGCCCAACAAGGACTGTTGAAATTATTA *****
DNA40981	2521	TGTGGATGATGAGATTACGGGAGACACACCCATGGAAAGCCACCTGCCATGCCTGCTAT *****
P_AAA77596	2521	TGTGGATGATGAGATTACGGGAGACACACCCATGGAAAGCCACCTGCCATGCCTGCTAT *****
DNA40981	2581	CGAGCATGAGCACCTAAATCACTATAACTCATACAAATCTCCCTCAACCACACAAC *****
P_AAA77596	2581	CGAGCATGAGCACCTAAATCACTATAACTCATACAAATCTCCCTCAACCACACAAC *****
DNA40981	2641	AGTTAACACAATAAATTCAATACACAGTTCACTGCAGTGAACCGTTATTGATCCGAATGAA *****
P_AAA77596	2641	AGTTAACACAATAAATTCAATACACAGTTCACTGCAGTGAACCGTTATTGATCCGAATGAA *****
DNA40981	2701	CTCTAAAGACAATGTACAAGAGACTCAAATCTAAACATTTACAGAGTTACAAAAAACAA *****
P_AAA77596	2701	CTCTAAAGACAATGTACAAGAGACTCAAATCTAAACATTTACAGAGTTACAAAAAACAA *****
DNA40981	2761	ACAATCAAAAAAGACAGTTATTAAAAATGACACAAATGACTGGCTAAATCTACTG *****
P_AAA77596	2761	ACAATCAAAAAAGACAGTTATTAAAAATGACACAAATGACTGGCTAAATCTACTG *****
DNA40981	2821	TTTCAAAAAAGTGTCTTACAAAAACAAAAAGAAAAGAAATTATTATTAAAAATT *****
P_AAA77596	2821	TTTCAAAAAAGTGTCTTACAAAAACAAAAAGAAAAGAAATTATTATTAAAAATT *****
DNA40981	2881	CTATTGTGATCTAAAGCAGACAAAAA *****
P_AAA77596	2881	CTATTGTGATCTAAAGCAGACAAAAA *****

>6 P\_AAX52265 Protein PRO331 cDNA clone DNA40981-1234. DNA, PAT 25-JUN-1999  
(2906 bp) [1 seg]  
Score = 2906 (5761 bits), Expect = 0.0

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PART DESEN A-17

Identities = 2906/2906 (100%), at 1,1-2906,2906, Strand +/+

DNA40981	1	GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTGGTGGTGGCTGTTGGG *****
P_AAX52265	1	GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTGGTGGTGGCTGTTGGG *****
DNA40981	61	TGCCTTGCAAAATGAAGGATGCAGGACGCAGCTTCCTCGAACCGAACGCAATGGAT *****
P_AAX52265	61	TGCCTTGCAAAATGAAGGATGCAGGACGCAGCTTCCTCGAACCGAACGCAATGGAT *****
DNA40981	121	AAACTGATTGTGCAAGAGAGAAGGAAGAACGAAGCTTTCTTGTGAGCCCTGGATCTTA *****
P_AAX52265	121	AAACTGATTGTGCAAGAGAGAAGGAAGAACGAAGCTTTCTTGTGAGCCCTGGATCTTA *****
DNA40981	181	ACACAAATGTGTATATGTGCACACAGGGAGCATTCAAGAACGAAATAACCAGAGTTAGA *****
P_AAX52265	181	ACACAAATGTGTATATGTGCACACAGGGAGCATTCAAGAACGAAATAACCAGAGTTAGA *****
DNA40981	241	CCCGCGGGGGTTGGTGTGTTCTGACATAAAATAATCTTAAAGCAGCTGTTCCCTCC *****
P_AAX52265	241	CCCGCGGGGGTTGGTGTGTTCTGACATAAAATAATCTTAAAGCAGCTGTTCCCTCC *****
DNA40981	301	CCACCCCCAAAAAAAGGATGATTGGAAATGAAGAACCGAGGATTCACAAAGAAAAAGT *****
P_AAX52265	301	CCACCCCCAAAAAAAGGATGATTGGAAATGAAGAACCGAGGATTCACAAAGAAAAAGT *****
DNA40981	361	ATGTTCATTTTCTCTATAAAGGAGAAAGTGAGCCAAGGAGATATTTTGGAAATGAAAAG *****
P_AAX52265	361	ATGTTCATTTTCTCTATAAAGGAGAAAGTGAGCCAAGGAGATATTTTGGAAATGAAAAG *****
DNA40981	421	TTTGGGGCTTTTAGTAAAGTAAAGAACCTGGTGTGGTGGTTTCCCTTTCTTTGAA *****
P_AAX52265	421	TTTGGGGCTTTTAGTAAAGTAAAGAACCTGGTGTGGTGGTTTCCCTTTCTTTGAA *****
DNA40981	481	TTTCCCACAAGAGGAGAGGAATTAAATAATACATCTGCAAAGAAATTTCAGAGAACAAAA *****
P_AAX52265	481	TTTCCCACAAGAGGAGAGGAATTAAATAATACATCTGCAAAGAAATTTCAGAGAACAAAA *****
DNA40981	541	GTTGACCGCGGCAGATTGAGGCATTGATTGGGGAGAGAACCCAGCAGAGCACAGTTGGA *****
P_AAX52265	541	GTTGACCGCGGCAGATTGAGGCATTGATTGGGGAGAGAACCCAGCAGAGCACAGTTGGA *****
DNA40981	601	TTTGTGCCATGTTGACTAAATTGACGGATAATTGCAGTTGGATTTCTTCATCAACC *****
P_AAX52265	601	TTTGTGCCATGTTGACTAAATTGACGGATAATTGCAGTTGGATTTCTTCATCAACC *****
DNA40981	661	TCCTTTTTAAATTTTATTCTTTGGTATCAAGATCATGCGTTTCTCTTGTCTT *****
P_AAX52265	661	TCCTTTTTAAATTTTATTCTTTGGTATCAAGATCATGCGTTTCTCTTGTCTT *****
DNA40981	721	AACCACCTGGATTCCATCTGGATGTTGCTGTGATCAGTCTGAAATACAACGTGGAAAT *****
P_AAX52265	721	AACCACCTGGATTCCATCTGGATGTTGCTGTGATCAGTCTGAAATACAACGTGGAAAT *****
DNA40981	781	TCCAGAAGGACCAACACCAGATAATTATGAATGTTGAACAAAGATGACCTTACATCCACA *****
P_AAX52265	781	TCCAGAAGGACCAACACCAGATAATTATGAATGTTGAACAAAGATGACCTTACATCCACA *****
DNA40981	841	GCAGATAATGATAGGTCCCTAGGTTAACAGGGCCCTATTGACCCCTGCTTGTGGTGC *****
P_AAX52265	841	GCAGATAATGATAGGTCCCTAGGTTAACAGGGCCCTATTGACCCCTGCTTGTGGTGC *****
DNA40981	901	GCTGGCTCTCAACTCTTGTGGCTGGCTGGTGCAGACCTGCCCTCTGT *****

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BLAST RESULTS A-16

P\_AAX52265 901 GCTGGCTTCAACTCTTGTGGTGGCTGGCTGGTCAGACCTGCCCTCTGT  
DNA40981 961 GTGCTCCTGCAGCAACCAGTTCAAGCAAGGTGATTGTGTTCGAAAAACCTGCGTGAGGT  
\*\*\*\*\*  
P\_AAX52265 961 GTGCTCCTGCAGCAACCAGTTCAAGCAAGGTGATTGTGTTCGAAAAACCTGCGTGAGGT  
DNA40981 1021 TCCGGATGGCATCTCCACCAACACACGGCTGCTGAACCTCCATGAGAACCAAATCCAGAT  
\*\*\*\*\*  
P\_AAX52265 1021 TCCGGATGGCATCTCCACCAACACACGGCTGCTGAACCTCCATGAGAACCAAATCCAGAT  
DNA40981 1081 CATCAAAGTGAACAGCTTCAAGCACTTGAGGCACTGGAAATCCTACAGTTGAGTAGGAA  
\*\*\*\*\*  
P\_AAX52265 1081 CATCAAAGTGAACAGCTTCAAGCACTTGAGGCACTGGAAATCCTACAGTTGAGTAGGAA  
DNA40981 1141 CCATATCAGAACCATGAAATTGGGGCTTCAATGGTCTGGCGAACCTAACACTCTGGA  
\*\*\*\*\*  
P\_AAX52265 1141 CCATATCAGAACCATGAAATTGGGGCTTCAATGGTCTGGCGAACCTAACACTCTGGA  
DNA40981 1201 ACTCTTGACAATCGTCTTACCATCCGAATGGAGCTTTGTATACTTGTCTAAACT  
\*\*\*\*\*  
P\_AAX52265 1201 ACTCTTGACAATCGTCTTACCATCCGAATGGAGCTTTGTATACTTGTCTAAACT  
DNA40981 1261 GAAGGAGCTCTGGTGCAGAACACCCCCATTGAAAGCATTGCTTATGCTTTAACAG  
\*\*\*\*\*  
P\_AAX52265 1261 GAAGGAGCTCTGGTGCAGAACACCCCCATTGAAAGCATTGCTTATGCTTTAACAG  
DNA40981 1321 AATTCTCTTGCAGCGACTAGACTTAGGGGAATTGAAAAGACTTTCATACATCTCAGA  
\*\*\*\*\*  
P\_AAX52265 1321 AATTCTCTTGCAGCGACTAGACTTAGGGGAATTGAAAAGACTTTCATACATCTCAGA  
DNA40981 1381 AGGTGCCTTGAAGGTCTGTCAACTTGAGGTATTGAAACCTTGCATGTGCAACCTTCG  
\*\*\*\*\*  
P\_AAX52265 1381 AGGTGCCTTGAAGGTCTGTCAACTTGAGGTATTGAAACCTTGCATGTGCAACCTTCG  
DNA40981 1441 GGAAATCCCTAACCTCACACCGCTCATAAAAGTAGATGAGCTGGATTTCTGGAAATCA  
\*\*\*\*\*  
P\_AAX52265 1441 GGAAATCCCTAACCTCACACCGCTCATAAAAGTAGATGAGCTGGATTTCTGGAAATCA  
DNA40981 1501 TTTATCTGCCATCAGGCCTGGCTTTCCAGGGTTGATGCACCTTCAGTGGAT  
\*\*\*\*\*  
P\_AAX52265 1501 TTTATCTGCCATCAGGCCTGGCTTTCCAGGGTTGATGCACCTTCAGTGGAT  
DNA40981 1561 GATACAGTCCCAGATTCAAGTGATTGAACCGGAATGCCCTTGACAACCTTCAGTCAGT  
\*\*\*\*\*  
P\_AAX52265 1561 GATACAGTCCCAGATTCAAGTGATTGAACCGGAATGCCCTTGACAACCTTCAGTCAGT  
DNA40981 1621 GGAGATCAACCTGGCACACAATACTAACATTACTGCCTCATGACCTTCACTCCCTT  
\*\*\*\*\*  
P\_AAX52265 1621 GGAGATCAACCTGGCACACAATACTAACATTACTGCCTCATGACCTTCACTCCCTT  
DNA40981 1681 GCATCATCTAGAGCGGATACATTACATCACACCCCTGGAACTGTAAGTGTGACATAC  
\*\*\*\*\*  
P\_AAX52265 1681 GCATCATCTAGAGCGGATACATTACATCACACCCCTGGAACTGTAAGTGTGACATAC  
DNA40981 1741 GTGGCTCAGCTGGGATAAAAGACATGGCCCCCTCGAACACAGCTTGTGCCCCGGTG  
\*\*\*\*\*  
P\_AAX52265 1741 GTGGCTCAGCTGGGATAAAAGACATGGCCCCCTCGAACACAGCTTGTGCCCCGGTG  
DNA40981 1801 TAACACTCCTCCCAATCTAAAGGGGAGGTACATTGGAGAGCTCGACCAGAATTACTTCAC  
\*\*\*\*\*  
P\_AAX52265 1801 TAACACTCCTCCCAATCTAAAGGGGAGGTACATTGGAGAGCTCGACCAGAATTACTTCAC  
DNA40981 1861 ATGCTATGCTCCGGTGAATTGTGGAGCCCCCTGCAGACCTCAATGTCAGTGAAGGCATGGC  
\*\*\*\*\*

BAC/ST RESULTS A-19

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P_AAX52265	1861	ATGCTATGCTCCGGTATTGTGGAGCCCCCTGCAGACCTCAATGTCACTGAAGGCATGGC
DNA40981	1921	AGCTGAGCTGAAATGTCGGCCTCCACATCCCCTGACATCTGTATCTGGATTACTCCAAA
P_AAX52265	1921	AGCTGAGCTGAAATGTCGGCCTCCACATCCCCTGACATCTGTATCTGGATTACTCCAAA
DNA40981	1981	TGGAACAGTCATGACACATGGGGCGTACAAAGTGGGATAGCTGTGCTCAGTGATGGTAC
P_AAX52265	1981	TGGAACAGTCATGACACATGGGGCGTACAAAGTGGGATAGCTGTGCTCAGTGATGGTAC
DNA40981	2041	GTTAAATTCACAAATGTAAGTCACTGCAAGATAACAGGCATGTACACATGTATGGTGGTAA
P_AAX52265	2041	GTTAAATTCACAAATGTAAGTCACTGCAAGATAACAGGCATGTACACATGTATGGTGGTAA
DNA40981	2101	TTCCGTTGGAAATACTACTGCTTCAGCCACCCTGAATGTTACTGCAGCAACCAACTACTCC
P_AAX52265	2101	TTCCGTTGGAAATACTACTGCTTCAGCCACCCTGAATGTTACTGCAGCAACCAACTACTCC
DNA40981	2161	TTTCTCTTACTTTCAACCGTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGCACG
P_AAX52265	2161	TTTCTCTTACTTTCAACCGTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGCACG
DNA40981	2221	GACCACAGATAACAATGTGGGCCCCACTCCAGTGGTCGACTGGGAGACCACCAATGTGAC
P_AAX52265	2221	GACCACAGATAACAATGTGGGCCCCACTCCAGTGGTCGACTGGGAGACCACCAATGTGAC
DNA40981	2281	CACCTCTCTCACACCACAGAGCACAAGGTCGACAGAGAAAACCTTCACCATCCCAGTGAC
P_AAX52265	2281	CACCTCTCTCACACCACAGAGCACAAGGTCGACAGAGAAAACCTTCACCATCCCAGTGAC
DNA40981	2341	TGATATAAACAGTGGGATCCAGGAATTGATGAGGTCACTGAAGACTACCAAAATCATCAT
P_AAX52265	2341	TGATATAAACAGTGGGATCCAGGAATTGATGAGGTCACTGAAGACTACCAAAATCATCAT
DNA40981	2401	TGGGTGTTTGTGGCCATCACACTCATGGCTGCAGTGATGCTGGTCATTTCTACAAGAT
P_AAX52265	2401	TGGGTGTTTGTGGCCATCACACTCATGGCTGCAGTGATGCTGGTCATTTCTACAAGAT
DNA40981	2461	GAGGAAGCAGCACCATCGGAAAACCATCACGCCCAACAAGGACTGTTGAAATTATCAA
P_AAX52265	2461	GAGGAAGCAGCACCATCGGAAAACCATCACGCCCAACAAGGACTGTTGAAATTATCAA
DNA40981	2521	TGTGGATGATGAGATTACGGGAGACACACCCATGGAAAGCCACCTGCCATGCCTGCTAT
P_AAX52265	2521	TGTGGATGATGAGATTACGGGAGACACACCCATGGAAAGCCACCTGCCATGCCTGCTAT
DNA40981	2581	CGAGCATGAGCACCTAAATCACTATAACTCATACAAATCTCCCTTCAACCACACAAC
P_AAX52265	2581	CGAGCATGAGCACCTAAATCACTATAACTCATACAAATCTCCCTTCAACCACACAAC
DNA40981	2641	AGTTAACACAATAATTCAATACACAGTTCACTGACATGAACCGTTATTGATCCGAATGAA
P_AAX52265	2641	AGTTAACACAATAATTCAATACACAGTTCACTGACATGAACCGTTATTGATCCGAATGAA
DNA40981	2701	CTCTAAAGACAATGTACAAGAGACTCAAATCTAAACATTACAGAGTTACAAAAAACAA
P_AAX52265	2701	CTCTAAAGACAATGTACAAGAGACTCAAATCTAAACATTACAGAGTTACAAAAAACAA
DNA40981	2761	ACAATCAAAAAAAAGACAGTTATTAAAAATGACACAAATGACTGGGCTAAATCTACTG
P_AAX52265	2761	ACAATCAAAAAAAAGACAGTTATTAAAAATGACACAAATGACTGGGCTAAATCTACTG
DNA40981	2821	TTTCAAAAAAGTGTCTTACAAAAAAACAAAAAGAAAAAGAAAATTTATTAAAAATT

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BEST RESULTS A20

P\_AAX52265 2821 TTTCAAAAAAGTGTCTTACAAAAAAACAAAAAAGAAAAGAAATTATTATTAATT  
DNA40981 2881 CTATTGTGATCTAACAGCAGACAAAAA  
\*\*\*\*\*  
P\_AAX52265 2881 CTATTGTGATCTAACAGCAGACAAAAA  
  
>7 AX098385 Sequence 11 from Patent WO0119991. (2906 bp) [1 seg]  
Score = 2906 (5761 bits), Expect = 0.0  
Identities = 2906/2906 (100%), at 1,1-2906,2906, Strand +/  
  
DNA40981 1 GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTTTGGTGGTGGCTGTTGGG  
\*\*\*\*\*  
AX098385 1 GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTTTGGTGGTGGCTGTTGGG  
\*\*\*\*\*  
DNA40981 61 TGCCCTTGCAAAATGAAGGATGCAGGACGCAGCTTCCTCGAACCGAACGCAATGGAT  
\*\*\*\*\*  
AX098385 61 TGCCCTTGCAAAATGAAGGATGCAGGACGCAGCTTCCTCGAACCGAACGCAATGGAT  
\*\*\*\*\*  
DNA40981 121 AAACTGATTGTGCAAGAGAGAAGGAAGAACGAAAGCTTTCTTGTGAGCCCTGGATCTTA  
\*\*\*\*\*  
AX098385 121 AAACTGATTGTGCAAGAGAGAAGGAAGAACGAAAGCTTTCTTGTGAGCCCTGGATCTTA  
\*\*\*\*\*  
DNA40981 181 ACACAAATGTGTATATGTGCACACAGGGAGCATTCAAGAACGAAATAAACCAAGAGTTAGA  
\*\*\*\*\*  
AX098385 181 ACACAAATGTGTATATGTGCACACAGGGAGCATTCAAGAACGAAATAAACCAAGAGTTAGA  
\*\*\*\*\*  
DNA40981 241 CCCGCGGGGTTGGTGTGTTCTGACATAAATAATCTTAAAGCAGCTGTTCCCCCTCC  
\*\*\*\*\*  
AX098385 241 CCCGCGGGGTTGGTGTGTTCTGACATAAATAATCTTAAAGCAGCTGTTCCCCCTCC  
\*\*\*\*\*  
DNA40981 301 CCACCCCCAAAAAAAGGATGATTGAAATGAAGAACCGAGGATTCACAAAGAAAAAGT  
\*\*\*\*\*  
AX098385 301 CCACCCCCAAAAAAAGGATGATTGAAATGAAGAACCGAGGATTCACAAAGAAAAAGT  
\*\*\*\*\*  
DNA40981 361 ATGTTCATTTCTCTATAAAGGAGAAAGTGGCCAAGGAGATTTTGGAAATGAAAAG  
\*\*\*\*\*  
AX098385 361 ATGTTCATTTCTCTATAAAGGAGAAAGTGGCCAAGGAGATTTTGGAAATGAAAAG  
\*\*\*\*\*  
DNA40981 421 TTTGGGGCTTTTAGTAAAGTAAAGAACGTTGGTGTGGTGGTTTCTTCTTTGAA  
\*\*\*\*\*  
AX098385 421 TTTGGGGCTTTTAGTAAAGAACGTTGGTGTGGTGGTTTCTTCTTTGAA  
\*\*\*\*\*  
DNA40981 481 TTTCCCACAAGAGGAGAGGAATTAAATAACATCTGCAAAGAACATTTCAGAGAACAAAA  
\*\*\*\*\*  
AX098385 481 TTTCCCACAAGAGGAGAGGAATTAAATAACATCTGCAAAGAACATTTCAGAGAACAAAA  
\*\*\*\*\*  
DNA40981 541 GTTGACCGCGGCAGATTGAGGCATTGATTGGGGAGAGAACCCAGCAGAGCACAGTTGGA  
\*\*\*\*\*  
AX098385 541 GTTGACCGCGGCAGATTGAGGCATTGATTGGGGAGAGAACCCAGCAGAGCACAGTTGGA  
\*\*\*\*\*  
DNA40981 601 TTTGTGCCTATGTGACTAAATTGACGGATAATTGCAGTTGGATTTCTTCATCAACC  
\*\*\*\*\*  
AX098385 601 TTTGTGCCTATGTGACTAAATTGACGGATAATTGCAGTTGGATTTCTTCATCAACC  
\*\*\*\*\*  
DNA40981 661 TCCTTTTTAAATTTTATTCTTTGGTATCAAGATCATGCGTTTCTCTTGTCTT  
\*\*\*\*\*  
AX098385 661 TCCTTTTTAAATTTTATTCTTTGGTATCAAGATCATGCGTTTCTCTTGTCTT  
\*\*\*\*\*  
DNA40981 721 AACCACCTGGATTCCATCTGGATGTTGCTGTGATCAGTCTGAAATACAACACTGTTGAAT  
\*\*\*\*\*  
AX098385 721 AACCACCTGGATTCCATCTGGATGTTGCTGTGATCAGTCTGAAATACAACACTGTTGAAT  
\*\*\*\*\*  
DNA40981 781 TCCAGAAGGACCAACACCAGATAAAATTATGAATGTTGAACAAGATGACCTACATCCACA  
\*\*\*\*\*

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BLAST RESULTS A-21

AX098385	781	TCCAGAAGGACCAACACCAGATAAATTATGAATGTGAACAAGATGACCTTACATCCACA
DNA40981	841	GCAGATAATGATAGGCCTAGGTTAACAGGGCCCTATTGACCCCCTGCTGTGGTGC*
AX098385	841	GCAGATAATGATAGGCCTAGGTTAACAGGGCCCTATTGACCCCCTGCTGTGGTGC*
DNA40981	901	GCTGGCTCTTCACACTTCTGTGGTGGCTGGTCTGGTGCAGACCTGCCCTCTGT
AX098385	901	GCTGGCTCTTCACACTTCTGTGGTGGCTGGTCTGGTGCAGACCTGCCCTCTGT
DNA40981	961	GTGCTCCTGCAGCAACCAGTTCAGCAAGGTGATTGTGTTCGAAAAACCTGCGTGAGGT
AX098385	961	GTGCTCCTGCAGCAACCAGTTCAGCAAGGTGATTGTGTTCGAAAAACCTGCGTGAGGT
DNA40981	1021	TCCGGATGGCATCTCACCAACACACGGCTGCTGAACCTCCATGAGAACCAAATCCAGAT
AX098385	1021	TCCGGATGGCATCTCACCAACACACGGCTGCTGAACCTCCATGAGAACCAAATCCAGAT
DNA40981	1081	CATCAAAGTGAACAGCTCAAGCACTTGAGGCACTTGAAATCCTACAGTTGAGTAGGAA
AX098385	1081	CATCAAAGTGAACAGCTCAAGCACTTGAGGCACTTGAAATCCTACAGTTGAGTAGGAA
DNA40981	1141	CCATATCAGAACCAATTGAAATTGGGGCTTCATGGCTGGCGAACCTAACACTCTGGA
AX098385	1141	CCATATCAGAACCAATTGAAATTGGGGCTTCATGGCTGGCGAACCTAACACTCTGGA
DNA40981	1201	ACTCTTGACAATCGTCTTACCATCCCAGGATGGAGCTTTGTATACTGTCTAAACT
AX098385	1201	ACTCTTGACAATCGTCTTACCATCCCAGGATGGAGCTTTGTATACTGTCTAAACT
DNA40981	1261	GAAGGAGCTCTGGTGCAGAACACCCCCATTGAAAGCATCCCTCTATGCTTTAACAG
AX098385	1261	GAAGGAGCTCTGGTGCAGAACACCCCCATTGAAAGCATCCCTCTATGCTTTAACAG
DNA40981	1321	AATTCTCTTGCAGCGACTAGACTTAGGGGAATTGAAAAGACTTCATACATCTCAGA
AX098385	1321	AATTCTCTTGCAGCGACTAGACTTAGGGGAATTGAAAAGACTTCATACATCTCAGA
DNA40981	1381	AGGTGCCTTGAGGTCTGTCCAACTTGAGGTATTGAACCTGCCATGTGCAACCTCG
AX098385	1381	AGGTGCCTTGAGGTCTGTCCAACTTGAGGTATTGAACCTGCCATGTGCAACCTCG
DNA40981	1441	GGAAATCCCTAACCTCACACCGCTCATAAAAGACTAGATGAGCTGGATCTGGAAATCA
AX098385	1441	GGAAATCCCTAACCTCACACCGCTCATAAAAGACTAGATGAGCTGGATCTGGAAATCA
DNA40981	1501	TTTATCTGCCATCAGGCCTGGCTCTTCCAGGGTTGATGCACCTCAAAACTGTGGAT
AX098385	1501	TTTATCTGCCATCAGGCCTGGCTCTTCCAGGGTTGATGCACCTCAAAACTGTGGAT
DNA40981	1561	GATACAGTCCCAGATTCAAGTGATTGAACGGAATGCCTTGACACCTTCAGTCAGT
AX098385	1561	GATACAGTCCCAGATTCAAGTGATTGAACGGAATGCCTTGACACCTTCAGTCAGT
DNA40981	1621	GGAGATCAACCTGGCACACAATAATCTAACATTACTGCCTCATGACCTCTCACTCCCTT
AX098385	1621	GGAGATCAACCTGGCACACAATAATCTAACATTACTGCCTCATGACCTCTCACTCCCTT
DNA40981	1681	GCATCATCTAGAGCGGATACATTACATCACAAACCTTGGAACTGTAACGTGACATACT
AX098385	1681	GCATCATCTAGAGCGGATACATTACATCACAAACCTTGGAACTGTAACGTGACATACT
DNA40981	1741	GTGGCTCAGCTGGTGGATAAAAGACATGGCCCCCTCGAACACAGCTTGTGCCCCGTG

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AX098385 1741 GTGGCTCAGCTGGTGGATAAAAGACATGGCCCCCTGAACACAGCTGTTGTGCCCGGTG  
DNA40981 1801 TAACACTCCTCCCAATCTAAAGGGGAGGTACATTGGAGAGCTGACCAGAATTACTTCAC  
\*\*\*\*\*  
AX098385 1801 TAACACTCCTCCCAATCTAAAGGGGAGGTACATTGGAGAGCTGACCAGAATTACTTCAC  
DNA40981 1861 ATGCTATGCTCCGGTGATTGTGGAGCCCCCTGCAGACCTCAATGTCACTGAAGGCATGGC  
\*\*\*\*\*  
AX098385 1861 ATGCTATGCTCCGGTGATTGTGGAGCCCCCTGCAGACCTCAATGTCACTGAAGGCATGGC  
DNA40981 1921 AGCTGAGCTGAAATGTCGGGCCTCCACATCCCTGACATCTGTATCTGGATTACTCCAAA  
\*\*\*\*\*  
AX098385 1921 AGCTGAGCTGAAATGTCGGGCCTCCACATCCCTGACATCTGTATCTGGATTACTCCAAA  
DNA40981 1981 TGGAACAGTCATGACACATGGGGCGTACAAAGTGGGATAGCTGTGCTCAGTGATGGTAC  
\*\*\*\*\*  
AX098385 1981 TGGAACAGTCATGACACATGGGGCGTACAAAGTGGGATAGCTGTGCTCAGTGATGGTAC  
DNA40981 2041 GTTAAATTTCACAAATGTAAGTCACTGTGCAAGATAACAGGCATGTACACATGTATGGTGAGTAA  
\*\*\*\*\*  
AX098385 2041 GTTAAATTTCACAAATGTAAGTCACTGTGCAAGATAACAGGCATGTACACATGTATGGTGAGTAA  
DNA40981 2101 TTCCGTTGGAAATACTACTGCTTCAGCCACCCCTGAATGTTACTGCAGCAACCAACTACTCC  
\*\*\*\*\*  
AX098385 2101 TTCCGTTGGAAATACTACTGCTTCAGCCACCCCTGAATGTTACTGCAGCAACCAACTACTCC  
DNA40981 2161 TTTCTCTTACTTTCAACCGTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGCACG  
\*\*\*\*\*  
AX098385 2161 TTTCTCTTACTTTCAACCGTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGCACG  
DNA40981 2221 GACCACAGATAACAATGTGGTCCCCTCCAGTGGTCAGTGGGAGACCACCAATGTGAC  
\*\*\*\*\*  
AX098385 2221 GACCACAGATAACAATGTGGTCCCCTCCAGTGGTCAGTGGGAGACCACCAATGTGAC  
DNA40981 2281 CACCTCTCACACCAACAGAGCACAAGGTCGACAGAGAAAACCTTCACCATCCCAGTGAC  
\*\*\*\*\*  
AX098385 2281 CACCTCTCACACCAACAGAGCACAAGGTCGACAGAGAAAACCTTCACCATCCCAGTGAC  
DNA40981 2341 TGATATAAACAGTGGGATCCAGGAATTGATGAGGTCAAGAGACTACCAAAATCATCAT  
\*\*\*\*\*  
AX098385 2341 TGATATAAACAGTGGGATCCAGGAATTGATGAGGTCAAGAGACTACCAAAATCATCAT  
DNA40981 2401 TGGGTGTTTGTGGCCATCACACTCATGGCTGCAGTGATGCTGGTCATTTCTACAAGAT  
\*\*\*\*\*  
AX098385 2401 TGGGTGTTTGTGGCCATCACACTCATGGCTGCAGTGATGCTGGTCATTTCTACAAGAT  
DNA40981 2461 GAGGAAGCAGCACCATCGGCAAAACCATCACGCCCAACAAGGACTGTTGAAATTATTAA  
\*\*\*\*\*  
AX098385 2461 GAGGAAGCAGCACCATCGGCAAAACCATCACGCCCAACAAGGACTGTTGAAATTATTAA  
DNA40981 2521 TGTGGATGATGAGATTACGGGAGACACACCCATGGAAAGCCACCTGCCATGCCTGCTAT  
\*\*\*\*\*  
AX098385 2521 TGTGGATGATGAGATTACGGGAGACACACCCATGGAAAGCCACCTGCCATGCCTGCTAT  
DNA40981 2581 CGAGCATGAGCACCTAAATCACTATAACTCATACAAATCTCCCTCAACCACACAAC  
\*\*\*\*\*  
AX098385 2581 CGAGCATGAGCACCTAAATCACTATAACTCATACAAATCTCCCTCAACCACACAAC  
DNA40981 2641 AGTTAACACAATAATTCAATACACAGTTCACTGCAGTGAACCGTTATTGATCCGAATGAA  
\*\*\*\*\*  
AX098385 2641 AGTTAACACAATAATTCAATACACAGTTCACTGCAGTGAACCGTTATTGATCCGAATGAA  
DNA40981 2701 CTCTAAAGACAATGTACAAGAGACTCAAATCTAAACATTACAGAGTTACAAAAAACAA  
\*\*\*\*\*

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AX098385 2701 CTCTAAAGACAATGTACAAGAGACTCAAATCTAAAACATTACAGAGTTACAAAAAACAA  
DNA40981 2761 ACAATCAAAAAAAAGACAGT TTATTAAAAATGACACAAATGACTGGGCTAAATCTACTG  
\*\*\*\*\*  
AX098385 2761 ACAATCAAAAAAAAGACAGT TTATTAAAAATGACACAAATGACTGGGCTAAATCTACTG  
DNA40981 2821 TTTCAAAAAAGTGTCTTACAAAAAACA AAAAGAAAAGAAATT TATTAAAAATT  
\*\*\*\*\*  
AX098385 2821 TTTCAAAAAAGTGTCTTACAAAAAACA AAAAGAAAAGAAATT TATTAAAAATT  
DNA40981 2881 CTATTGTGATCTAAAGCAGACAAAAA  
\*\*\*\*\*  
AX098385 2881 CTATTGTGATCTAAAGCAGACAAAAA  
  
>8 AB046800 Homo sapiens mRNA for KIAA1580 protein, partial cds. (4055 bp) [1 seg]  
Score = 2889 (5727 bits), Expect = 0.0  
Identities = 2898/2901 (99%), at 1,1155-2901,4055, Strand +/-  
  
DNA40981 1 GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTTTGGTGGTGGCTGTTGGG  
\*\*\*\*\*  
AB046800 1155 GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTTTGGTGGTGGCTGTTGGG  
  
DNA40981 61 TGCC TTGCAAAATGAAGGATGCAGGACGCAGCTTCTCCTGGAACCGAACGCAATGGAT  
\*\*\*\*\*  
AB046800 1215 TGCC TTGCAAAATGAAGGATGCAGGACGCAGCTTCTCCTGGAACCGAACGCAATGGAT  
  
DNA40981 121 AAACTGATTGTGCAAGAGAGAAGGAAGAACGAAGCCTTTCTTGAGCCCTGGATCTTA  
\*\*\*\*\*  
AB046800 1275 AAACTGATTGTGCAAGAGAGAAGGAAGAACGAAGCCTTTCTTGAGCCCTGGATCTTA  
  
DNA40981 181 ACACAAATGTGTATATGTGCACACAGGGACATTCAAGAACGAAATAAACCAAGAGTTAGA  
\*\*\*\*\*  
AB046800 1335 ACACAAATGTGTATATGTGCACACAGGGACATTCAAGAACGAAATAAACCAAGAGTTAGA  
  
DNA40981 241 CCCGC GGTTGGTGTGTTCTGACATAAATAATCTTAAAGCAGCTGTTCCCTCC  
\*\*\*\*\*  
AB046800 1395 CCCGC GGTTGGTGTGTTCTGACATAAATAATCTTAAAGCAGCTGTTCCCTCC  
  
DNA40981 301 CCACCCCCAAAAAAAGGATGATTGGAAATGAAGAACGAGGATTCAAAAGAAAAAGT  
\*\*  
AB046800 1455 CCCCCCCC AAAAAAAGGATGATTGGAAATGAAGAACGAGGATTCAAAAGAAAAAGT  
  
DNA40981 361 ATGTTCATTTCTCTATAAAGGAGAAAGT GAGCCAAGGAGATATTTTGGAAATGAAAAG  
\*\*\*\*\*  
AB046800 1515 ATGTTCATTTCTCTATAAAGGAGAAAGT GAGCCAAGGAGATATTTTGGAAATGAAAAG  
  
DNA40981 421 TTTGGGGCTTTTAGTAAAGTAAAGAACGAGCTGGTGTGGTGGTGTCTTCTTTGAA  
\*\*\*\*\*  
AB046800 1575 TTTGGGGCTTTTAGTAAAGTAAAGAACGAGCTGGTGTGGTGGTGTCTTCTTTGAA  
  
DNA40981 481 TTTCCCACAAGAGGAGAGGAAATTAAATAACATCTGCAAAGAAATTCAAGAGAACAAAA  
\*\*\*\*\*  
AB046800 1635 TTTCCCACAAGAGGAGAGGAAATTAAATAACATCTGCAAAGAAATTCAAGAGAACAAAA  
  
DNA40981 541 GTTGACCGCGGCAGATTGAGGCATTGATTGGGGAGAGAACAGCACAGTGGA  
\*\*\*\*\*  
AB046800 1695 GTTGACCGCGGCAGATTGAGGCATTGATTGGGGAGAGAACAGCACAGTGGA  
  
DNA40981 601 TTTGTGCCTATGTTGACTAAATTGACGGATAATTGCAGTTGGATTTCATCAACC  
\*\*\*\*\*  
AB046800 1755 TTTGTGCCTATGTTGACTAAATTGACGGATAATTGCAGTTGGATTTCATCAACC  
  
DNA40981 661 TCCTTTTTAAATT TATTCCCTTGGTATCAAGATCATGCCTTCTCTTGTCTT

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AB046800	1815	***** TCCTTTTTAAATTATCCTTGGTATCAAGATCATGCGTTCTTGTCTT
DNA40981	721	***** AACCACCTGGATTCATCTGGATGTTGCTGTGATCAGTCTGAAATACA ACTGTTGAAT
AB046800	1875	***** AACCACCTGGATTCATCTGGATGTTGCTGTGATCAGTCTGAAATACA ACTGTTGAAT
DNA40981	781	***** TCCAGAAGGACCAACACCAGATAAAATTATGAATGTTGAACAAGATG ACCTACATCCACA
AB046800	1935	***** TCCAGAAGGACCAACACCAGATAAAATTATGAATGTTGAACAAGATG ACCTACATCCACA
DNA40981	841	***** GCAGATAATGATAGGTCTAGGTTAACAGGGCCCTATTGACCCCC TGCTGTGGTGCT
AB046800	1995	***** GCAGATAATGATAGGTCTAGGTTAACAGGGCCCTATTGACCCCC TGCTGTGGTGCT
DNA40981	901	***** GCTGGCTCTCAACTTCTTGTGGTGGCTGGCTGGTGC GGGCTCAGACCTGCCCTCTGT
AB046800	2055	***** GCTGGCTCTCAACTTCTTGTGGTGGCTGGTCTGGTGC GGGCTCAGACCTGCCCTCTGT
DNA40981	961	***** GTGCTCCTGCAGCAACCAGTTCAGCAAGGTGATTGTT CGGAAAAACCTGCGTGAGGT
AB046800	2115	***** GTGCTCCTGCAGCAACCAGTTCAGCAAGGTGATTGTT CGGAAAAACCTGCGTGAGGT
DNA40981	1021	***** TCCGGATGGCATCTCACCAACACACGGCTGCTGAAC CTCCATGAGAACCAAATCCAGAT
AB046800	2175	***** TCCGGATGGCATCTCACCAACACACGGCTGCTGAAC CTCCATGAGAACCAAATCCAGAT
DNA40981	1081	***** CATCAAAGTGAACAGCCTCAAGCA GACTTGAGGCACTTG GAGGAACTTGAA ACTTGAGTAGGAA
AB046800	2235	***** CATCAAAGTGAACAGCCTCAAGCA GACTTGAGGAACTTG GAGGAACTTGAA ACTTGAGTAGGAA
DNA40981	1141	***** CCATATCAGAACCAATTG GAAATTGGGGCTTCA ATGGCTGGCGAAC CTCAACACTCTGG A
AB046800	2295	***** CCATATCAGAACCAATTG GAAATTGGGGCTTCA ATGGCTGGCGAAC CTCAACACTCTGG A
DNA40981	1201	***** ACTCTTGACAATCGT TTACTACCATCCC GAATGGAGCTT GTATACTTG CTAAACT
AB046800	2355	***** ACTCTTGACAATCGT TTACTACCATCCC GAATGGAGCTT GTATACTTG CTAAACT
DNA40981	1261	***** GAAGGAGCTCTGG TGC GAAACAAC CCCCATTG AAAGCAT CCCTCTT ATGCTTT AACAG
AB046800	2415	***** GAAGGAGCTCTGG TGC GAAACAAC CCCCATTG AAAGCAT CCCTCTT ATGCTTT AACAG
DNA40981	1321	***** AATTCTTCTTGC GCCGACTAGACT TAGGGGAATTG AAAAGACT TTCATACAT CTCAGA
AB046800	2475	***** AATTCTTCTTGC GCCGACTAGACT TAGGGGAATTG AAAAGACT TTCATACAT CTCAGA
DNA40981	1381	***** AGGTGC CTTGAGGTCT GTCCA ACTTGAGGT ATTG AACCT TGCCAT GTGCA ACCTCG
AB046800	2535	***** AGGTGC CTTGAGGTCT GTCCA ACTTGAGGT ATTG AACCT TGCCAT GTGCA ACCTCG
DNA40981	1441	***** GGAAATCC CTAAC CTCAC ACCC GCT ATAAA ACTAGA TGAG GCTGG ATCTT CTGG AATCA
AB046800	2595	***** GGAAATCC CTAAC CTCAC ACCC GCT ATAAA ACTAGA TGAG GCTGG ATCTT CTGG AATCA
DNA40981	1501	***** TTTATCT GCCAT CAGGC CTGG CTTT CCAGGG TTG ATGC CAC CTCA AAA ACT GTGG AT
AB046800	2655	***** TTTATCT GCCAT CAGGC CTGG CTTT CCAGGG TTG ATGC CAC CTCA AAA ACT GTGG AT
DNA40981	1561	***** GATACAGT CCCAG ATTCA AGTG ATTG AAC GGA ATG CCTT GACA AC CT CAG TCA CTAG T
AB046800	2715	***** GATACAGT CCCAG ATTCA AGTG ATTG AAC GGA ATG CCTT GACA AC CT CAG TCA CTAG T
DNA40981	1621	***** GGAGAT CAAC CTGG CAC ACA ATA CTAAC ATT ACT GCCT CAT GAC CT TTCA CTCC CTT

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\*\*\*\*\*  
AB046800 2775 GGAGATCAACCTGGCACACAATAATCTAACATTACTGCCTCATGACCTTCACCCCTT  
DNA40981 1681 GCATCATCTAGAGCGGATACATTACATCACAAACCTTGGAACTGTAACTGTGACATACT  
\*\*\*\*\*  
AB046800 2835 GCATCATCTAGAGCGGATACATTACATCACAAACCTTGGAACTGTAACTGTGACATACT  
DNA40981 1741 GTGGCTCAGCTGGTGGATAAAAGACATGCCCTCGAACACAGCTGTTGTGCCCGGTG  
\*\*\*\*\*  
AB046800 2895 GTGGCTCAGCTGGTGGATAAAAGACATGCCCTCGAACACAGCTGTTGTGCCCGGTG  
DNA40981 1801 TAACACTCCTCCCAATCTAAAGGGGAGGTACATTGGAGAGCTCGACCAGAATTACTTCAC  
\*\*\*\*\*  
AB046800 2955 TAACACTCCTCCCAATCTAAAGGGGAGGTACATTGGAGAGCTCGACCAGAATTACTTCAC  
DNA40981 1861 ATGCTATGCTCCGGTGAATTGGAGCCCCCTGCAGACCTCAATGTCACTGAAGGCATGGC  
\*\*\*\*\*  
AB046800 3015 ATGCTATGCTCCGGTGAATTGGAGCCCCCTGCAGACCTCAATGTCACTGAAGGCATGGC  
DNA40981 1921 AGCTGAGCTGAAATGTCGGGCCTCCACATCCCTGACATCTGTATCTGGATTACTCCAAA  
\*\*\*\*\*  
AB046800 3075 AGCTGAGCTGAAATGTCGGGCCTCCACATCCCTGACATCTGTATCTGGATTACTCCAAA  
DNA40981 1981 TGGAACAGTCATGACACATGGGGCGTACAAAGTGGGATAGCTGTGCTCAGTGATGGTAC  
\*\*\*\*\*  
AB046800 3135 TGGAACAGTCATGACACATGGGGCGTACAAAGTGGGATAGCTGTGCTCAGTGATGGTAC  
DNA40981 2041 GTTAAATTTCACAAATGTAAGTGCAGACATGGGGCGTACAAAGTGGGATAGCTGTGCTCAGTGATGGTAA  
\*\*\*\*\*  
AB046800 3195 GTTAAATTTCACAAATGTAAGTGCAGACATGGGGCGTACAAAGTGGGATAGCTGTGCTCAGTGATGGTAA  
DNA40981 2101 TTCCGTTGGAAATACTACTGCTTCAGCCACCCCTGAATGTTACTGCAGCAACCACTACTCC  
\*\*\*\*\*  
AB046800 3255 TTCCGTTGGAAATACTACTGCTTCAGCCACCCCTGAATGTTACTGCAGCAACCACTACTCC  
DNA40981 2161 TTTCTCTTACTTTCAACCGTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGCACG  
\*\*\*\*\*  
AB046800 3315 TTTCTCTTACTTTCAACCGTCACAGTAGAGACTATGGAACCGTCTCAGGATGAGGCACG  
DNA40981 2221 GACCACAGATAACAATGTGGTCCCCTCCAGTGGTCGACTGGGAGACCACCAATGTGAC  
\*\*\*\*\*  
AB046800 3375 GACCACAGATAACAATGTGGTCCCCTCCAGTGGTCGACTGGGAGACCACCAATGTGAC  
DNA40981 2281 CACCTCTCTCACACCCACAGAGCACAGGTGACAGAGAAAAACCTTCACCATCCCAGTGAC  
\*\*\*\*\*  
AB046800 3435 CACCTCTCTCACACCCACAGAGCACAGGTGACAGAGAAAAACCTTCACCATCCCAGTGAC  
DNA40981 2341 TGATATAAACAGTGGGATCCCAAGGAATTGATGAGGTGATGAAGACTACCAAAATCATCAT  
\*\*\*\*\*  
AB046800 3495 TGATATAAACAGTGGGATCCCAAGGAATTGATGAGGTGATGAAGACTACCAAAATCATCAT  
DNA40981 2401 TGGGTGTTTGTGGCCATCACACTCATGGCTGCAGTGATGCTGGTCATTTCTACAAGAT  
\*\*\*\*\*  
AB046800 3555 TGGGTGTTTGTGGCCATCACACTCATGGCTGCAGTGATGCTGGTCATTTCTACAAGAT  
DNA40981 2461 GAGGAAGCAGCACCATCGGAAACACATCACGCCAACAGGACTGTTGAAATTATCAA  
\*\*\*\*\*  
AB046800 3615 GAGGAAGCAGCACCATCGGAAACACATCACGCCAACAGGACTGTTGAAATTATCAA  
DNA40981 2521 TGTGGATGATGAGATTACGGGAGACACACCCATGGAAAGCCACCTGCCATGCCTGCTAT  
\*\*\*\*\*  
AB046800 3675 TGTGGATGATGAGATTACGGGAGACACACCCATGGAAAGCCACCTGCCATGCCTGCTAT  
DNA40981 2581 CGAGCATGAGCACCTAAACTACTACATAACTACAAATCTCCCTCAACCACACAAC

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\*\*\*\*\*  
AB046800 3735 CGAGCATGAGCACCTAAATCACTATAACTACATAACAAATCTCCCTCAACCACACAAC  
DNA40981 2641 AGTTAACACAATAAATTCAATACACAGTCAGTCAGTCAGTCAGTCATGAACCGTTATTGATCCGAATGAA  
\*\*\*\*\*  
AB046800 3795 AGTTAACACAATAAATTCAATACACAGTCAGTCAGTCAGTCATGAACCGTTATTGATCCGAATGAA  
DNA40981 2701 CTCTAAAGACAATGTACAAGAGACTCAAATCTAAAACATTACAGAGTTACAAAAAACAA  
\*\*\*\*\*  
AB046800 3855 CTCTAAAGACAATGTACAAGAGACTCAAATCTAAAACATTACAGAGTTACAAAAAACAA  
DNA40981 2761 ACAATCAAAAAAAAGACAGTTATTAAAAATGACACAAATGACTGGGCTAAATCTACTG  
\*\*\*\*\*  
AB046800 3915 ACAATCAAAAAAAAGACAGTTATTAAAAATGACACAAATGACTGGGCTAAATCTACTG  
DNA40981 2821 TTTCAAAAAAGTGTCTTACAAAAAAACAAAAAGAAAAGAAATTTATTAAAAATT  
\*\*\*\*\*  
AB046800 3975 TTTCAAAAAAGTGTCTTACAAAAAAACAAAAAGAAAAGAAATTTATTAAAAATT  
DNA40981 2881 CTATTGTGATCTAACAGCAGAC  
\*\*\*\*\*  
AB046800 4035 CTATTGTGATCTAACAGCAGAC  
  
>9 AC021820 Homo sapiens clone RP11-40H19, WORKING DRAFT SEQUENCE, 11 unordered  
(157201 bp) [1 seg]  
Score = 2136 (4234 bits), Expect = 0.0  
Identities = 2136/2136 (100%), at 770,28891-2905,31026, Strand +/  
  
DNA40981 770 ACTGTTGAATTCCAGAAGGCCAACACCCAGATAAATTATGAATGTTGAACAAAGATGACC  
\*\*\*\*\*  
AC021820 28891 ACTGTTGAATTCCAGAAGGCCAACACCCAGATAAATTATGAATGTTGAACAAAGATGACC  
DNA40981 830 TTACATCCACAGCAGATAATGATAGGTCTAGGTTAACAGGCCCTATTGACCCCCCTG  
\*\*\*\*\*  
AC021820 28951 TTACATCCACAGCAGATAATGATAGGTCTAGGTTAACAGGCCCTATTGACCCCCCTG  
DNA40981 890 CTTGTGGTGCTGGCTCTCAACTTCTGTGGCTGGCTGGTCTGGTCAGGCTCAGACC  
\*\*\*\*\*  
AC021820 29011 CTTGTGGTGCTGGCTCTCAACTTCTGTGGCTGGCTGGTCTGGTCAGGCTCAGACC  
DNA40981 950 TGCCCTCTGTGCTGCCTGCAGCAACCAGTCAGCAAGGTGATTGTTCGGAAAAAC  
\*\*\*\*\*  
AC021820 29071 TGCCCTCTGTGCTGCCTGCAGCAACCAGTCAGCAAGGTGATTGTTCGGAAAAAC  
DNA40981 1010 CTGCGTGAGGTTCCGGATGGCATCTCCACCAACACAGGCTGCTGAACCTCCATGAGAAC  
\*\*\*\*\*  
AC021820 29131 CTGCGTGAGGTTCCGGATGGCATCTCCACCAACACAGGCTGCTGAACCTCCATGAGAAC  
DNA40981 1070 CAAATCCAGATCATCAAAGTGAACAGCAGCTCAAGCAGTCAGTCAGCAAGGTGATTGTTCGGAAAAAC  
\*\*\*\*\*  
AC021820 29191 CAAATCCAGATCATCAAAGTGAACAGCAGCTCAAGCAGTCAGTCAGCAAGGTGATTGTTCGGAAAAAC  
DNA40981 1130 TTGAGTAGGAACCATACTCAGAACCATATTGAAATTGGGGTTCAATGGTCTGGCGAACCTC  
\*\*\*\*\*  
AC021820 29251 TTGAGTAGGAACCATACTCAGAACCATATTGAAATTGGGGTTCAATGGTCTGGCGAACCTC  
DNA40981 1190 AACACTCTGGAACTCTTGACAATCGTCTACTACCATCCCGAATGGAGCTTTGTATAC  
\*\*\*\*\*  
AC021820 29311 AACACTCTGGAACTCTTGACAATCGTCTACTACCATCCCGAATGGAGCTTTGTATAC  
DNA40981 1250 TTGTCTAAACTGAAGGAGCTGGTTGCGAACACACCCATTGAAAGCATCCCTTCTTAT  
\*\*\*\*\*  
AC021820 29371 TTGTCTAAACTGAAGGAGCTGGTTGCGAACACACCCATTGAAAGCATCCCTTCTTAT

DNA40981	1310	GCTTTAACAGAACATTCTTGCAGCCACTAGACTTAGGGAAATTGAAAAGACTTCA *****
AC021820	29431	GCTTTAACAGAACATTCTTGCAGCCACTAGACTTAGGGAAATTGAAAAGACTTCA
DNA40981	1370	TACATCTCAGAACGGTGCCTTGAGGTCTGTCCAACTTGAGGTATTGAACCTGCCATG *****
AC021820	29491	TACATCTCAGAACGGTGCCTTGAGGTCTGTCCAACTTGAGGTATTGAACCTGCCATG
DNA40981	1430	TGCAACCTCGGGAAATCCCTAACCTCACACCGCTCATAAAACAGATGAGCTGGATCTT *****
AC021820	29551	TGCAACCTCGGGAAATCCCTAACCTCACACCGCTCATAAAACAGATGAGCTGGATCTT
DNA40981	1490	TCTGGGAATCATTATCTGCCATCAGGCCCTGGCTTTCCAGGGTTGATGCACCTTCAA *****
AC021820	29611	TCTGGGAATCATTATCTGCCATCAGGCCCTGGCTTTCCAGGGTTGATGCACCTTCAA
DNA40981	1550	AAACTGTGGATGATACTAGTCCCAGATTCAAGTGATTGAACGGAATGCCTTGACAACCTT *****
AC021820	29671	AAACTGTGGATGATACTAGTCCCAGATTCAAGTGATTGAACGGAATGCCTTGACAACCTT
DNA40981	1610	CAGTCACTAGTGGAGATCAACCTGGCACACAATAATCTAACATTACTGCCATGACCTC *****
AC021820	29731	CAGTCACTAGTGGAGATCAACCTGGCACACAATAATCTAACATTACTGCCATGACCTC
DNA40981	1670	TTCACTCCCTTGACATCATCTAGAGCGGATACATTACATCACAAACCCTGGAACGTAAAC *****
AC021820	29791	TTCACTCCCTTGACATCATCTAGAGCGGATACATTACATCACAAACCCTGGAACGTAAAC
DNA40981	1730	TGTGACATACTGTGGCTCAGCTGGTGGATAAAAGACATGGCCCCCTCGAACACAGCTGT *****
AC021820	29851	TGTGACATACTGTGGCTCAGCTGGTGGATAAAAGACATGGCCCCCTCGAACACAGCTGT
DNA40981	1790	TGTGCCCGGTGTAACACTCCTCCAACTAAAGGGGAGGTACATTGGAGAGCTGACCGAG *****
AC021820	29911	TGTGCCCGGTGTAACACTCCTCCAACTAAAGGGGAGGTACATTGGAGAGCTGACCGAG
DNA40981	1850	AATTACTTCACATGCTATGCTCCGGTGATTGTGGAGCCCCCTGCAGACCTCAATGTCACT *****
AC021820	29971	AATTACTTCACATGCTATGCTCCGGTGATTGTGGAGCCCCCTGCAGACCTCAATGTCACT
DNA40981	1910	GAAGGCATGGCAGCTGAGCTGAAATGTCGGGCTCCACATCCCTGACATCTGTATCTGG *****
AC021820	30031	GAAGGCATGGCAGCTGAGCTGAAATGTCGGGCTCCACATCCCTGACATCTGTATCTGG
DNA40981	1970	ATTACTCCAAATGGAACAGTCATGACACATGGGGCGTACAAAGTGCAGGATAGCTGTGCTC *****
AC021820	30091	ATTACTCCAAATGGAACAGTCATGACACATGGGGCGTACAAAGTGCAGGATAGCTGTGCTC
DNA40981	2030	AGTGATGGTACGTTAATTTCACAAATGTAACACTGTGCAAGACATAGGCATGTACACATGT *****
AC021820	30151	AGTGATGGTACGTTAATTTCACAAATGTAACACTGTGCAAGACATAGGCATGTACACATGT
DNA40981	2090	ATGGTGAGTAATTCCGTTGGAAACTACTGCTTCAGCCACCTGAATGTTACTGCAGCA *****
AC021820	30211	ATGGTGAGTAATTCCGTTGGAAACTACTGCTTCAGCCACCTGAATGTTACTGCAGCA
DNA40981	2150	ACCAACTACTCCTTCTTTACTTTCAACCGTCACAGTAGAGACTATGGAACCGTCTCAG *****
AC021820	30271	ACCAACTACTCCTTCTTTACTTTCAACCGTCACAGTAGAGACTATGGAACCGTCTCAG
DNA40981	2210	GATGAGGCACGGACCACAGATAACATGGGGTCCCCTCCAGTGGTCGACTGGGAGACC *****
AC021820	30331	GATGAGGCACGGACCACAGATAACATGGGGTCCCCTCCAGTGGTCGACTGGGAGACC

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SMAI DRAFT

DNA40981	2270	ACCAATGTGACCACCTCTCACACCACAGAGCACAAGGTCGACAGAGAAAACCTTCACC
AC021820	30391	ACCAATGTGACCACCTCTCACACCACAGAGCACAAGGTCGACAGAGAAAACCTTCACC
DNA40981	2330	ATCCCAGTGACTGATATAAACAGTGGGATCCCAGGAATTGATGAGGTCATGAAGACTACC
AC021820	30451	ATCCCAGTGACTGATATAAACAGTGGGATCCCAGGAATTGATGAGGTCATGAAGACTACC
DNA40981	2390	AAAATCATCATTGGGTGTTTGTGCCATCACACTCATGGCTGCAGTGATGCTGGTCATT
AC021820	30511	AAAATCATCATTGGGTGTTTGTGCCATCACACTCATGGCTGCAGTGATGCTGGTCATT
DNA40981	2450	TTCTACAAGATGAGGAAGCAGCACCATCGGCAAACCATCACGCCCAACAAGGACTGTT
AC021820	30571	TTCTACAAGATGAGGAAGCAGCACCATCGGCAAACCATCACGCCCAACAAGGACTGTT
DNA40981	2510	GAAATTATAATGTGGATGATGAGATTACGGGAGACACACCCATGGAAAGGCCACCTGCC
AC021820	30631	GAAATTATAATGTGGATGATGAGATTACGGGAGACACACCCATGGAAAGGCCACCTGCC
DNA40981	2570	ATGCCTGCTATCGAGCATGAGCACCTAAATCACTATAACTCATACAAATCTCCCTCAAC
AC021820	30691	ATGCCTGCTATCGAGCATGAGCACCTAAATCACTATAACTCATACAAATCTCCCTCAAC
DNA40981	2630	CACACAACAACAGTTAACACAATAAATTCAATACACAGTTCACTGCATGAACCGTTATTG
AC021820	30751	CACACAACAACAGTTAACACAATAAATTCAATACACAGTTCACTGCATGAACCGTTATTG
DNA40981	2690	ATCCGAATGAACTCTAAAGACAATGTACAAGAGACTCAAATCTAAAACATTACAGAGTT
AC021820	30811	ATCCGAATGAACTCTAAAGACAATGTACAAGAGACTCAAATCTAAAACATTACAGAGTT
DNA40981	2750	ACAAAAAAACAACATCAAAAAAAAGACAGTTATTAAAAATGACACAAATGACTGGGC
AC021820	30871	ACAAAAAAACAACATCAAAAAAAAGACAGTTATTAAAAATGACACAAATGACTGGGC
DNA40981	2810	TAAATCTACTGTTCAAAAAAGTGTCTTACAAAAAAACAAAAAGAAAAGAAATTATT
AC021820	30931	TAAATCTACTGTTCAAAAAAGTGTCTTACAAAAAAACAAAAAGAAAAGAAATTATT
DNA40981	2870	TATTAaaaATTCTATTGTGATCTAAAGCAGACAAAA
AC021820	30991	TATTAaaaATTCTATTGTGATCTAAAGCAGACAAAA

>10 AC080100 Homo sapiens chromosome 11 clone RP11-454H19 map 11, WORKING DRAFT  
(151999 bp) [1 seg]

Score = 2132 (4226 bits), Expect = 0.0

Identities = 2135/2136 (99%), at 770,22645-2905,20510, Strand +/-

DNA40981	770	ACTGTTGAATTCCAGAAGGACCAACACCAGATAAAATTATGAATGTTGAACAAGATGACC
AC080100	22645	ACTGTTGAATTCCAGAAGGACCAACACCAGATAAAATTATGAATGTTGAACAAGATGACC
DNA40981	830	TTACATCCACAGCAGATAATGATAGGTCTAGGTTAACAGGGCCCTATTGACCCCTG
AC080100	22585	TTACATCCACAGCAGATAATGATAGGTCTAGGTTAACAGGGCCCTATTGACCCCTG
DNA40981	890	CTTGTGGTGCTGGCTTCAACTTCTTGTGGTGGCTGGCTGGTGCAGACC
AC080100	22525	CTTGTGGTGCTGGCTTCAACTTCTTGTGGTGGCTGGCTGGTGCAGACC
DNA40981	950	TGCCCTCTGTGTGCTCCTGCAGCAACCAGTTCAGCAAGGTGATTGTGTTCGGAAAAAC
AC080100	22465	TGCCCTCTGTGTGCTCCTGCAGCAACCAGTTCAGCAAGGTGATTGTGTTCGGAAAAAC

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BLAST RESULTS A-29

DNA40981	1010	CTGCGTAGGGTCCGGATGGCATCTCCACCAACACACGGCTGCTGAACCTCCATGAGAAC
AC080100	22405	*****
DNA40981	1070	CAAATCCAGATCATCAAAGTGAACAGCAGCTCAAGCACTTGAGGCACTTGGAAATCCTACAG
AC080100	22345	*****
DNA40981	1130	TTGAGTAGGAACCATACTAGAACATTGAAATTGGGGCTTCATGGTCTGGCGAACCTC
AC080100	22285	*****
DNA40981	1190	AACACTCTGGAACTCTTGACAATCGTCTACTACCATCCCAGATGGAGCTTTGTATAC
AC080100	22225	*****
DNA40981	1250	TTGTCTAAACTGAAGGAGCTGGTGCAGAACACCCCCATTGAAAGCATTCCCTTCTTAT
AC080100	22165	*****
DNA40981	1310	GCTTTAACAGAATTCTCTTGCAGCCACTAGACTTAGGGAAATTGAAAAGACTTTCA
AC080100	22105	*****
DNA40981	1370	TACATCTCAGAACGGTGCCTTGAGGTCTGTCCAACTTGAGGTATTGAAACCTGCCATG
AC080100	22045	*****
DNA40981	1430	TGCAACCTCGGGAAATCCCTAACCTCACACCGCTCATAAAAGTGAACCTGGATCTT
AC080100	21985	*****
DNA40981	1490	TCTGGGAATCATTATCTGCCATCAGGCCCTGGCTTTCCAGGGTTGATGCACCTTCAA
AC080100	21925	*****
DNA40981	1550	AAACTGTGGATGATACTGGCAGATTCAAGTGATTGAACGGATGCCCTTGACAACCTT
AC080100	21865	*****
DNA40981	1610	CAGTCACTAGTGGAGATCAACCTGGCACACAATAATCTAACATTACTGCCCTCATGACCTC
AC080100	21805	*****
DNA40981	1670	TTCACTCCCTGACATCTAGAGCGGATACATTACATCACAAACCTGGAACTGTAAC
AC080100	21745	*****
DNA40981	1730	TGTGACATACTGTGGCTCAGCTGGGATAAAAGACATGGCCCCCTGAAACACAGCTGTG
AC080100	21685	*****
DNA40981	1790	TGTGCCCGGTGTAACACTCCTCCAACTAAAGGGGAGGTACATTGGAGAGCTCGACCAAG
AC080100	21625	*****
DNA40981	1850	AATTACTTCACATGCTATGCTCCGGTGATTGTGGAGCCCCCTGCAGACCTCAATGTCACT
AC080100	21565	*****
DNA40981	1910	GAAGGCATGGCAGCTGAGCTGAAATGTCGGGCCTCCACATCCCTGACATCTGTATCTGG
AC080100	21505	*****

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RESULTS A-30

DNA40981 1970 ATTACTCCAAATGGAACAGTCATGACACATGGGGCGTACAAAGTAGCTGTGCTC  
\*\*\*\*\*  
AC080100 21445 ATTACTCCAAATGGAACAGTCATGACACATGGGGCGTACAAAGTAGCTGTGCTC  
\*\*\*\*\*  
DNA40981 2030 AGTGATGGTACGTTAATTCAAAATGTAACGTGCAAGATAACAGGCATGTACACATGT  
\*\*\*\*\*  
AC080100 21385 AGTGATGGTACGTTAATTCAAAATGTAACGTGCAAGATAACAGGCATGTACACATGT  
\*\*\*\*\*  
DNA40981 2090 ATGGTGAGTAATTCCGTTGGGAATACTACTGCTTCAGCCACCCCTGAATGTTACTGCAGCA  
\*\*\*\*\*  
AC080100 21325 ATGGTGAGTAATTCCGTTGGGAATACTACTGCTTCAGCCACCCCTGAATGTTACTGCAGCA  
\*\*\*\*\*  
DNA40981 2150 ACCACTACTCCTTCCTTCAACCGTCACAGTAGAGACTATGGAACCGTCTCAG  
\*\*\*\*\*  
AC080100 21265 ACCACTACTCCTTCCTTCAACCGTCACAGTAGAGACTATGGAACCGTCTCAG  
\*\*\*\*\*  
DNA40981 2210 GATGAGGCACGGACCACAGATAACAATGTGGGTCCCCTCCAGTGGTCGACTGGGAGACC  
\*\*\*\*\*  
AC080100 21205 GATGAGGCACGGACCACAGATAACAATGTGGGTCCCCTCCAGTGGTCGACTGGGAGACC  
\*\*\*\*\*  
DNA40981 2270 ACCAATGTGACCACCTCTCACACCACAGAGCACAAGGTCGACAGAGAAAACCTTCACC  
\*\*\*\*\*  
AC080100 21145 ACCAATGTGACCACCTCTCACACCACAGAGCACAAGGTCGACAGAGAAAACCTTCACC  
\*\*\*\*\*  
DNA40981 2330 ATCCCAGTGAATGATATAAACAGTGGGATCCCAGGAATTGATGAGGTCATGAAGACTACC  
\*\*\*\*\*  
AC080100 21085 ATCCCAGTGAATGATATAAACAGTGGGATCCCAGGAATTGATGAGGTCATGAAGACTACC  
\*\*\*\*\*  
DNA40981 2390 AAAATCATCATTGGGTGTTTGTGCCATCACACTCATGGCTGCAGTGCTGGTCATT  
\*\*\*\*\*  
AC080100 21025 AAAATCATCATTGGGTGTTTGTGCCATCACACTCATGGCTGCAGTGCTGGTCATT  
\*\*\*\*\*  
DNA40981 2450 TTCTACAAGATGAGGAAGCAGCACCATCGGAAAACCACATCACGCCCAACAAGGACTGTT  
\*\*\*\*\*  
AC080100 20965 TTCTACAAGATGAGGAAGCAGCACCATCGGAAAACCACATCACGCCCAACAAGGACTGTT  
\*\*\*\*\*  
DNA40981 2510 GAAATTATTAATGTGGATGATGAGATTACGGGAGACACACCCATGGAAAGCCACCTGCC  
\*\*\*\*\*  
AC080100 20905 GAAATTATTAATGTGGATGATGAGATTACGGGAGACACACCCATGGAAAGCCACCTGCC  
\*\*\*\*\*  
DNA40981 2570 ATGCCTGCTATCGAGCATGAGCACCTAAATCACTATAACTCATACAAATCTCCCTTCAAC  
\*\*\*\*\*  
AC080100 20845 ATGCCTGCTATCGAGCATGAGCACCTAAATCACTATAACTCATACAAATCTCCCTTCAAC  
\*\*\*\*\*  
DNA40981 2630 CACACAACAAACAGTTAACACAATAAATTCAATACACAGTTCACTGCATGAACCGTTATTG  
\*\*\*\*\*  
AC080100 20785 CACACAACAAACAGTTAACACAATAAATTCAATACACAGTTCACTGCATGAACCGTTATTG  
\*\*\*\*\*  
DNA40981 2690 ATCCGAATGAACCTCAAAGACAATGTACAAGAGAGCTCAAATCTAAAACATTACAGAGTT  
\*\*\*\*\*  
AC080100 20725 ATCCGAATGAACCTCAAAGACAATGTACAAGAGAGCTCAAATCTAAAACATTACAGAGTT  
\*\*\*\*\*  
DNA40981 2750 ACAAAAAACAAACATCAAAAAAGACAGTTATTAAAAATGACACAAATGACTGGGC  
\*\*\*\*\*  
AC080100 20665 ACAAAAAACAAACATCAAAAAAGACAGTTATTAAAAATGACACAAATGACTGGGC  
\*\*\*\*\*  
DNA40981 2810 TAAATCTACTGTTCAAAAAGTGTCTTACAAAAAAACAAAAAGAAAAGAAATTATT  
\*\*\*\*\*  
AC080100 20605 TAAATCTACTGTTCAAAAAGTGTCTTACAAAAAAACAAAAAGAAAAGAAATTATT  
\*\*\*\*\*  
DNA40981 2870 TATTAACATTCTATTGTGATCTAAAGCAGACAAAA  
\*\*\*\*\*  
AC080100 20545 TATTAACATTCTATTGTGATCTAAAGCAGACAAAA

(B)

Blast Results 8-1

Tue Jul 17 13:25:41 2001 [BLASTP 2.1.3 [Apr-1-2001], NCBI]  
/home/ruby/va/Molbio/carpenda/temp1/p1.DNA40981 (640 aa)

Sequences producing High-scoring Segment Pairs:

			Score	Match	Pct	E-val
1	P_AAB53089	Human angiogenesis-associated protein PRO3	3362	640	100	0.0
2	P_AAB65292	Human PRO331 protein sequence SEQ ID NO:50	3362	640	100	0.0
3	P_AAB80262	Human PRO331 protein - Homo sapiens.	3362	640	100	0.0
4	P_AAY70673	Human PRO331 protein - Homo sapiens.	3362	640	100	0.0
5	P_AAB24407	Human PRO331 protein sequence SEQ ID NO:10	3362	640	100	0.0
6	P_AAY13394	protein PRO331 - Homo sapiens.	3362	640	100	0.0
7	P_AAW85722	Novel protein (Clone AS209_1) - Homo sapie	3362	640	100	0.0
8	P_AAY08100	Human PRO331 protein - Homo sapiens.	3362	640	100	0.0
9	BAB13406.1	KIAA1580 protein - Homo sapiens	3362	640	100	0.0

>1 P\_AAB53089 Human angiogenesis-associated protein PRO331, SEQ ID NO:137 - Homo sapiens. (640 aa) [1 seg]

Score = 3362 (1299 bits), Expect = 0.0

Identities = 640/640 (100%), Positives = 640/640 (100%), at 1,1-640,640

DNA40981	1	MLNKMTLHPQQIMIGPRFNRALFDPLLVLLALQLLVAGLVRAQTCPSVCSCSNQFSKV *****
P_AAB53089	1	MLNKMTLHPQQIMIGPRFNRALFDPLLVLLALQLLVAGLVRAQTCPSVCSCSNQFSKV *****
DNA40981	61	ICVRKNLREVPGDISTNTRLLNLHENQIQQIKVNSFKHLRHLEILQLSRNHIRTIEIGAF *****
P_AAB53089	61	ICVRKNLREVPGDISTNTRLLNLHENQIQQIKVNSFKHLRHLEILQLSRNHIRTIEIGAF *****
DNA40981	121	NGLANLNTLELFNDNRLTTIPNGAFVYLSKLKELWLRLNNPIESIPSYAFNRIPSLRRLDLG *****
P_AAB53089	121	NGLANLNTLELFNDNRLTTIPNGAFVYLSKLKELWLRLNNPIESIPSYAFNRIPSLRRLDLG *****
DNA40981	181	ELKRLSYISEGAFEGLSNLRYLNLCNLREIPNLPLIKLDELDLSGNHLSAIRPGSFQ *****
P_AAB53089	181	ELKRLSYISEGAFEGLSNLRYLNLCNLREIPNLPLIKLDELDLSGNHLSAIRPGSFQ *****
DNA40981	241	GLMHLQKLWMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPPLHHLERIHLHH *****
P_AAB53089	241	GLMHLQKLWMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPPLHHLERIHLHH *****
DNA40981	301	NPWCNCIDILWLSWWIKDMAPSNTACCACNTPPNLKGRYIGELDQNYFTCYAPVIVEPP *****
P_AAB53089	301	NPWCNCIDILWLSWWIKDMAPSNTACCACNTPPNLKGRYIGELDQNYFTCYAPVIVEPP *****
DNA40981	361	ADLNVTGMAAEALKCRASTSLSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVQD *****
P_AAB53089	361	ADLNVTGMAAEALKCRASTSLSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVQD *****
DNA40981	421	TGMYTCMVSNSVGNTTASATLNVTAAATTPFSYFSTVTVETMEPSQDEARTTDNNVGPTP *****
P_AAB53089	421	TGMYTCMVSNSVGNTTASATLNVTAAATTPFSYFSTVTVETMEPSQDEARTTDNNVGPTP *****
DNA40981	481	VVDWETTNVTTSLTPQSTRSTEKTFTIPVTDINSGIPGIDEVMKTTKIIIGCFVAITLMA *****
P_AAB53089	481	VVDWETTNVTTSLTPQSTRSTEKTFTIPVTDINSGIPGIDEVMKTTKIIIGCFVAITLMA *****
DNA40981	541	AVMLVIFYKMRKQHHRQNHAPTRTVEIINVDEITGDTPMESHLPMPAIEHEHLNHYNS

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\*\*\*\*\*  
P\_AAB53089 541 AVMLVIFYKMRKQHHRQNHHAPTRTVEIINVDEITGDTPMESHLPMPAIEHEHLNHYNS  
DNA40981 601 YKSPFNHTTVNTINSIHSSVHEPLLIRMNSKDNVQETQI  
\*\*\*\*\*  
P\_AAB53089 601 YKSPFNHTTVNTINSIHSSVHEPLLIRMNSKDNVQETQI  
  
>2 P\_AAB65292 Human PRO331 protein sequence SEQ ID NO:501 - Homo sapiens. (640 aa) [1 seg]  
Score = 3362 (1299 bits), Expect = 0.0  
Identities = 640/640 (100%), Positives = 640/640 (100%), at 1,1-640,640  
  
DNA40981 1 MLNKMTLHPQQIMIGPRFNRALFDPLLVLALLQQLVVAGLVRAQTCPSVCSCSNQFSKV  
\*\*\*\*\*  
P\_AAB65292 1 MLNKMTLHPQQIMIGPRFNRALFDPLLVLALLQQLVVAGLVRAQTCPSVCSCSNQFSKV  
  
DNA40981 61 ICVRKNLREVPGISTNTRLLNLHENQIQIIKVNSFKHLRHLEILQLSRNHIRTIEIGAF  
\*\*\*\*\*  
P\_AAB65292 61 ICVRKNLREVPGISTNTRLLNLHENQIQIIKVNSFKHLRHLEILQLSRNHIRTIEIGAF  
  
DNA40981 121 NGLANLNTLELFDNRLTTIPNGAFVYLSKLKEWLWLRNNPIESIPSYAFNRIPSLRRLDLG  
\*\*\*\*\*  
P\_AAB65292 121 NGLANLNTLELFDNRLTTIPNGAFVYLSKLKEWLWLRNNPIESIPSYAFNRIPSLRRLDLG  
  
DNA40981 181 ELKRLSYISEGAFEGLSNLRYLNLCNLREIPNLTPLIKLDDELDSGNHLSAIRPGSFQ  
\*\*\*\*\*  
P\_AAB65292 181 ELKRLSYISEGAFEGLSNLRYLNLCNLREIPNLTPLIKLDDELDSGNHLSAIRPGSFQ  
  
DNA40981 241 GLMHQKLWMIQSQIQVIERNNAFDNLQLSVEINLAHNNLTLLPHDLFTPPLHHLERIHLHH  
\*\*\*\*\*  
P\_AAB65292 241 GLMHQKLWMIQSQIQVIERNNAFDNLQLSVEINLAHNNLTLLPHDLFTPPLHHLERIHLHH  
  
DNA40981 301 NPWCNCNDILWLWSWIKD MAPSNTACCRCNTPPNLKGRYIGELDQNYFTCYAPVIVEPP  
\*\*\*\*\*  
P\_AAB65292 301 NPWCNCNDILWLWSWIKD MAPSNTACCRCNTPPNLKGRYIGELDQNYFTCYAPVIVEPP  
  
DNA40981 361 ADLNTEGMAAEKCRASTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVQD  
\*\*\*\*\*  
P\_AAB65292 361 ADLNTEGMAAEKCRASTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVQD  
  
DNA40981 421 TGYTCMVSNSVGNTTASATLNTAATTTPFSYFSTVTVETMEPSQDEARTTDNNVGPTP  
\*\*\*\*\*  
P\_AAB65292 421 TGYTCMVSNSVGNTTASATLNTAATTTPFSYFSTVTVETMEPSQDEARTTDNNVGPTP  
  
DNA40981 481 VVDWETTNVTTSLTPQSTRSTEKTFTIPVTDINSGIPGIDEVMKTTKIIIGCFVAITLMA  
\*\*\*\*\*  
P\_AAB65292 481 VVDWETTNVTTSLTPQSTRSTEKTFTIPVTDINSGIPGIDEVMKTTKIIIGCFVAITLMA  
  
DNA40981 541 AVMLVIFYKMRKQHHRQNHHAPTRTVEIINVDEITGDTPMESHLPMPAIEHEHLNHYNS  
\*\*\*\*\*  
P\_AAB65292 541 AVMLVIFYKMRKQHHRQNHHAPTRTVEIINVDEITGDTPMESHLPMPAIEHEHLNHYNS  
  
DNA40981 601 YKSPFNHTTVNTINSIHSSVHEPLLIRMNSKDNVQETQI  
\*\*\*\*\*  
P\_AAB65292 601 YKSPFNHTTVNTINSIHSSVHEPLLIRMNSKDNVQETQI  
  
>3 P\_AAB80262 Human PRO331 protein - Homo sapiens. (640 aa) [1 seg]

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BLAST RESULTS P-3

Score = 3362 (1299 bits), Expect = 0.0  
Identities = 640/640 (100%), Positives = 640/640 (100%), at 1,1-640,640

DNA40981 1 MLNKMTLHPQQIMIGPRFNRALFDPLLVLLALQLLVVAGLVRAQTCPSVCSCSNQFSKV  
\*\*\*\*\*  
P\_AAB80262 1 MLNKMTLHPQQIMIGPRFNRALFDPLLVLLALQLLVVAGLVRAQTCPSVCSCSNQFSKV  
\*\*\*\*\*  
DNA40981 61 ICVRKNLREVPGISTNTRLLNLHENQIQQIKVNSFKHLRHLEILQLSRNHIRTIEIGAF  
\*\*\*\*\*  
P\_AAB80262 61 ICVRKNLREVPGISTNTRLLNLHENQIQQIKVNSFKHLRHLEILQLSRNHIRTIEIGAF  
\*\*\*\*\*  
DNA40981 121 NGLANLNTLELFDNRLTTIPNGAFVYLSKLKEWLRLNNPIESIPSYAFNRIPSLRRLDLG  
\*\*\*\*\*  
P\_AAB80262 121 NGLANLNTLELFDNRLTTIPNGAFVYLSKLKEWLRLNNPIESIPSYAFNRIPSLRRLDLG  
\*\*\*\*\*  
DNA40981 181 ELKRLSYISEGAFEGLSNLRYLNLCNLREIPNLTPLIKLDLDELDLSGNHLSAIRPGSFQ  
\*\*\*\*\*  
P\_AAB80262 181 ELKRLSYISEGAFEGLSNLRYLNLCNLREIPNLTPLIKLDLDELDLSGNHLSAIRPGSFQ  
\*\*\*\*\*  
DNA40981 241 GLMHLQKLWMIQSQIQVIERNAFDNLQLSVEINLAHNNLTLLPHDLFTPPLHHLERIHLHH  
\*\*\*\*\*  
P\_AAB80262 241 GLMHLQKLWMIQSQIQVIERNAFDNLQLSVEINLAHNNLTLLPHDLFTPPLHHLERIHLHH  
\*\*\*\*\*  
DNA40981 301 NPWCNCIDILWLSWWIKDMAPSNTACCACRNTPNLKGRYIGELDQNYFTCYAPVIVEPP  
\*\*\*\*\*  
P\_AAB80262 301 NPWCNCIDILWLSWWIKDMAPSNTACCACRNTPNLKGRYIGELDQNYFTCYAPVIVEPP  
\*\*\*\*\*  
DNA40981 361 ADLNTEGMAAEELKCRASTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVQD  
\*\*\*\*\*  
P\_AAB80262 361 ADLNTEGMAAEELKCRASTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVQD  
\*\*\*\*\*  
DNA40981 421 TGMYTCMVSNSVGNTTASATLNTAATTPFSYFSTVTVETMEPSQDEARTTDNNVGPTP  
\*\*\*\*\*  
P\_AAB80262 421 TGMYTCMVSNSVGNTTASATLNTAATTPFSYFSTVTVETMEPSQDEARTTDNNVGPTP  
\*\*\*\*\*  
DNA40981 481 VVDWETTNVTTSLTPQSTRSTEKTFTIPVTDINSIGIPGIDEVMKTTKIIIGCFVAITLMA  
\*\*\*\*\*  
P\_AAB80262 481 VVDWETTNVTTSLTPQSTRSTEKTFTIPVTDINSIGIPGIDEVMKTTKIIIGCFVAITLMA  
\*\*\*\*\*  
DNA40981 541 AVMLVIFYKMRKQHHRQNHHAPTRTVEIINVDDIEITGDTPMESHLPMPAIEHEHLNHYS  
\*\*\*\*\*  
P\_AAB80262 541 AVMLVIFYKMRKQHHRQNHHAPTRTVEIINVDDIEITGDTPMESHLPMPAIEHEHLNHYS  
\*\*\*\*\*  
DNA40981 601 YKSPFNHTTVNTINSIHSSVHEPLLIRMNSKDNVQETQI  
\*\*\*\*\*  
P\_AAB80262 601 YKSPFNHTTVNTINSIHSSVHEPLLIRMNSKDNVQETQI

>4 P\_AAY70673 Human PRO331 protein - Homo sapiens. (640 aa) [1 seg]  
Score = 3362 (1299 bits), Expect = 0.0  
Identities = 640/640 (100%), Positives = 640/640 (100%), at 1,1-640,640

DNA40981 1 MLNKMTLHPQQIMIGPRFNRALFDPLLVLLALQLLVVAGLVRAQTCPSVCSCSNQFSKV  
\*\*\*\*\*  
P\_AAY70673 1 MLNKMTLHPQQIMIGPRFNRALFDPLLVLLALQLLVVAGLVRAQTCPSVCSCSNQFSKV  
\*\*\*\*\*  
DNA40981 61 ICVRKNLREVPGISTNTRLLNLHENQIQQIKVNSFKHLRHLEILQLSRNHIRTIEIGAF  
\*\*\*\*\*

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BLAST RESULTS B-A

P\_AAY70673 61 ICVRKNLREVPGISTNTRLLNLHENQIQQIKVNSFKHLRHLEILQLSRNHIRTIEIGAF  
DNA40981 121 NGLANLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPSLRRLDLG  
\*\*\*\*\*  
P\_AAY70673 121 NGLANLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPSLRRLDLG  
DNA40981 181 ELKRLSYISEGAFEGLSNLRYLNLCNLREIPNLTPLIKLDELDLSGNHLSAIRPGSFQ  
\*\*\*\*\*  
P\_AAY70673 181 ELKRLSYISEGAFEGLSNLRYLNLCNLREIPNLTPLIKLDELDLSGNHLSAIRPGSFQ  
DNA40981 241 GLMHLQKLWMIQSQIQVIERNAFDNLQLSVEINLAHNNLTLPHDLFTPPLHHLERIHLHH  
\*\*\*\*\*  
P\_AAY70673 241 GLMHLQKLWMIQSQIQVIERNAFDNLQLSVEINLAHNNLTLPHDLFTPPLHHLERIHLHH  
DNA40981 301 NPWCNCNDILWLSSWIKDMSNTACCACNTPPNLKGRYIGELDQNYFTCYAPVIVEPP  
\*\*\*\*\*  
P\_AAY70673 301 NPWCNCNDILWLSSWIKDMSNTACCACNTPPNLKGRYIGELDQNYFTCYAPVIVEPP  
DNA40981 361 ADLNTEGMAELKCRASTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVQD  
\*\*\*\*\*  
P\_AAY70673 361 ADLNTEGMAELKCRASTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVQD  
DNA40981 421 TGYTCMVSNVGNTTASATLNTAATTTPFSYFSTVTVETMEPSQDEARTTDNNVGPTP  
\*\*\*\*\*  
P\_AAY70673 421 TGYTCMVSNVGNTTASATLNTAATTTPFSYFSTVTVETMEPSQDEARTTDNNVGPTP  
DNA40981 481 VVDWETTNVTTSLTPQSTRSTEKTFTIPVTDINSGIPGIDEVMKTTKIIIGCFVAITLMA  
\*\*\*\*\*  
P\_AAY70673 481 VVDWETTNVTTSLTPQSTRSTEKTFTIPVTDINSGIPGIDEVMKTTKIIIGCFVAITLMA  
DNA40981 541 AVMLVIFYKMRKQHHRQNHHAPTRTVEIINVDEITGDPMEHLPMPAIEHEHLHNYS  
\*\*\*\*\*  
P\_AAY70673 541 AVMLVIFYKMRKQHHRQNHHAPTRTVEIINVDEITGDPMEHLPMPAIEHEHLHNYS  
DNA40981 601 YKSPFNHTTVNTINSIHSSVHEPLLIRMNSKDNVQETQI  
\*\*\*\*\*  
P\_AAY70673 601 YKSPFNHTTVNTINSIHSSVHEPLLIRMNSKDNVQETQI

>5 P\_AAB24407 Human PRO331 protein sequence SEQ ID NO:107 - Homo sapiens. (64 aa) [1 seg]

Score = 3362 (1299 bits), Expect = 0.0

Identities = 640/640 (100%), Positives = 640/640 (100%), at 1,1-640,640

DNA40981 1 MLNKMTLHPQQIMIGPRFNRALFDPLLVLVLLALQLLVAGLVRQAQTCPSVCSCSNQFSKV  
\*\*\*\*\*  
P\_AAB24407 1 MLNKMTLHPQQIMIGPRFNRALFDPLLVLVLLALQLLVAGLVRQAQTCPSVCSCSNQFSKV  
DNA40981 61 ICVRKNLREVPGISTNTRLLNLHENQIQQIKVNSFKHLRHLEILQLSRNHIRTIEIGAF  
\*\*\*\*\*  
P\_AAB24407 61 ICVRKNLREVPGISTNTRLLNLHENQIQQIKVNSFKHLRHLEILQLSRNHIRTIEIGAF  
DNA40981 121 NGLANLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPSLRRLDLG  
\*\*\*\*\*  
P\_AAB24407 121 NGLANLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPSLRRLDLG  
DNA40981 181 ELKRLSYISEGAFEGLSNLRYLNLCNLREIPNLTPLIKLDELDLSGNHLSAIRPGSFQ  
\*\*\*\*\*

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S-8  
SNSA TSME

P\_AAB24407 181 ELKRLSYISEGAFEGLSNLRYLNLCNLREIPNLTPLIKLDELDLSGNHLSAIRPGSFQ  
DNA40981 241 GLMHLQKLWMIQSQIQVIERNAFDNLQLSLVEINLAHNNLTLLPHDLFTPPLHHLERIHLHH  
\*\*\*\*\*  
P\_AAB24407 241 GLMHLQKLWMIQSQIQVIERNAFDNLQLSLVEINLAHNNLTLLPHDLFTPPLHHLERIHLHH  
DNA40981 301 NPWCNCNDILWLSSWIKDMAPSNTACCACNTPPNLKGRYIGELDQNYFTCYAPVIVEPP  
\*\*\*\*\*  
P\_AAB24407 301 NPWCNCNDILWLSSWIKDMAPSNTACCACNTPPNLKGRYIGELDQNYFTCYAPVIVEPP  
DNA40981 361 ADLNVTATEGMAELKCRASTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVQD  
\*\*\*\*\*  
P\_AAB24407 361 ADLNVTATEGMAELKCRASTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVQD  
DNA40981 421 TGMYTCMVSNSVGNTTASATLNVTAATTPFSYFSTVTVETMEPSQDEARTTDNNVGPTP  
\*\*\*\*\*  
P\_AAB24407 421 TGMYTCMVSNSVGNTTASATLNVTAATTPFSYFSTVTVETMEPSQDEARTTDNNVGPTP  
DNA40981 481 VVDWETTNVTTSLTPQSTRSTEKTFTIPVTDINSGIPGIDEVMKTTKIIIGCFVAITLMA  
\*\*\*\*\*  
P\_AAB24407 481 VVDWETTNVTTSLTPQSTRSTEKTFTIPVTDINSGIPGIDEVMKTTKIIIGCFVAITLMA  
DNA40981 541 AVMLVIFYKMRKQHHRQNHHAPTRTVEIINVDDIEITGDTPMESHLPMPAIEHEHLNHYS  
\*\*\*\*\*  
P\_AAB24407 541 AVMLVIFYKMRKQHHRQNHHAPTRTVEIINVDDIEITGDTPMESHLPMPAIEHEHLNHYS  
DNA40981 601 YKSPFNHTTVNTINSIHSSVHEPLLIRMNSKDNVQETQI  
\*\*\*\*\*  
P\_AAB24407 601 YKSPFNHTTVNTINSIHSSVHEPLLIRMNSKDNVQETQI  
  
>6 P\_AAY13394 protein PRO331 - Homo sapiens. (640 aa) [1 seg]  
Score = 3362 (1299 bits), Expect = 0.0  
Identities = 640/640 (100%), Positives = 640/640 (100%), at 1,1-640,640  
  
DNA40981 1 MLNKMTLHPQQIMIGPRFNRALFDPLLVLALQLLVAGLVRQAQTCPSVCSCSNQFSKV  
\*\*\*\*\*  
P\_AAY13394 1 MLNKMTLHPQQIMIGPRFNRALFDPLLVLALQLLVAGLVRQAQTCPSVCSCSNQFSKV  
DNA40981 61 ICVRKNLREVPGISTNTRLLNLHENQIQQIKVNSFKHLRHLEILQLSRNHIRTIEIGAF  
\*\*\*\*\*  
P\_AAY13394 61 ICVRKNLREVPGISTNTRLLNLHENQIQQIKVNSFKHLRHLEILQLSRNHIRTIEIGAF  
DNA40981 121 NGLANLNTLELFNRLLTIPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPSLRRLDLG  
\*\*\*\*\*  
P\_AAY13394 121 NGLANLNTLELFNRLLTIPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPSLRRLDLG  
DNA40981 181 ELKRLSYISEGAFEGLSNLRYLNLCNLREIPNLTPLIKLDELDLSGNHLSAIRPGSFQ  
\*\*\*\*\*  
P\_AAY13394 181 ELKRLSYISEGAFEGLSNLRYLNLCNLREIPNLTPLIKLDELDLSGNHLSAIRPGSFQ  
DNA40981 241 GLMHLQKLWMIQSQIQVIERNAFDNLQLSLVEINLAHNNLTLLPHDLFTPPLHHLERIHLHH  
\*\*\*\*\*  
P\_AAY13394 241 GLMHLQKLWMIQSQIQVIERNAFDNLQLSLVEINLAHNNLTLLPHDLFTPPLHHLERIHLHH  
DNA40981 301 NPWCNCNDILWLSSWIKDMAPSNTACCACNTPPNLKGRYIGELDQNYFTCYAPVIVEPP  
\*\*\*\*\*  
P\_AAY13394 301 NPWCNCNDILWLSSWIKDMAPSNTACCACNTPPNLKGRYIGELDQNYFTCYAPVIVEPP

BLAST RESULTS B-4

DNA40981 361 ADLNTEGMAAEKCRASTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTQD  
\*\*\*\*\*  
P\_AAY13394 361 ADLNTEGMAAEKCRASTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTQD  
  
DNA40981 421 TGMYTCMVSNSVGNTTASATLNVTAATTPFSYFSTVTVETMEPSQDEARTTDNNVGPTP  
\*\*\*\*\*  
P\_AAY13394 421 TGMYTCMVSNSVGNTTASATLNVTAATTPFSYFSTVTVETMEPSQDEARTTDNNVGPTP  
  
DNA40981 481 VVDWETTNVTTSLPQSTRSTEKTFTIPVTDINSGIPGIDEVMKTTKIIIGCFVAITLMA  
\*\*\*\*\*  
P\_AAY13394 481 VVDWETTNVTTSLPQSTRSTEKTFTIPVTDINSGIPGIDEVMKTTKIIIGCFVAITLMA  
  
DNA40981 541 AVMLVIFYKMRKQHHRQNHHAPTRTVEIINVDEITGDTPMESHLPMPAIEHEHLNHYNS  
\*\*\*\*\*  
P\_AAY13394 541 AVMLVIFYKMRKQHHRQNHHAPTRTVEIINVDEITGDTPMESHLPMPAIEHEHLNHYNS  
  
DNA40981 601 YKSPFNHTTVNTINSIHSSVHEPLLIRMNSKDNVQETQI  
\*\*\*\*\*  
P\_AAY13394 601 YKSPFNHTTVNTINSIHSSVHEPLLIRMNSKDNVQETQI  
  
>7 P\_AAW85722 Novel protein (Clone AS209\_1) - Homo sapiens. (640 aa) [1 seg]  
Score = 3362 (1299 bits), Expect = 0.0  
Identities = 640/640 (100%), Positives = 640/640 (100%), at 1,1-640,640  
  
DNA40981 1 MLNKMTLHPQQIMIGPRFNRALFDPLLVLLALQLLVAGLVRAQTCPSVCSCSNQFSKV  
\*\*\*\*\*  
P\_AAW85722 1 MLNKMTLHPQQIMIGPRFNRALFDPLLVLLALQLLVAGLVRAQTCPSVCSCSNQFSKV  
  
DNA40981 61 ICVRKNLREVPDGISTNTRLLNLHENQIQIICKVNSFKHLRHLIELQLSRNHIRTIEIGAF  
\*\*\*\*\*  
P\_AAW85722 61 ICVRKNLREVPDGISTNTRLLNLHENQIQIICKVNSFKHLRHLIELQLSRNHIRTIEIGAF  
  
DNA40981 121 NGLANLNTLELFNDNRLTTIPNGAFVYLSKLKEWLWRNNPIESIPSYAFNRIPSLRRLDLG  
\*\*\*\*\*  
P\_AAW85722 121 NGLANLNTLELFNDNRLTTIPNGAFVYLSKLKEWLWRNNPIESIPSYAFNRIPSLRRLDLG  
  
DNA40981 181 ELKRLSYISEGAFEGLSNLRYLNLCNLREIPNLPLIKLDELDLSGNHLSAIRPGSFQ  
\*\*\*\*\*  
P\_AAW85722 181 ELKRLSYISEGAFEGLSNLRYLNLCNLREIPNLPLIKLDELDLSGNHLSAIRPGSFQ  
  
DNA40981 241 GLMHLQKLWMIQSQIQVIERNAFDNLQLSVEINLAHNNLTLLPHDLFTPPLHHLERIHLHH  
\*\*\*\*\*  
P\_AAW85722 241 GLMHLQKLWMIQSQIQVIERNAFDNLQLSVEINLAHNNLTLLPHDLFTPPLHHLERIHLHH  
  
DNA40981 301 NPWCNCNDILWLWSWIKD MAPSNTACCACNTPPNLKGRYIGELDQNYFTCYAPVIVEPP  
\*\*\*\*\*  
P\_AAW85722 301 NPWCNCNDILWLWSWIKD MAPSNTACCACNTPPNLKGRYIGELDQNYFTCYAPVIVEPP  
  
DNA40981 361 ADLNTEGMAAEKCRASTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTQD  
\*\*\*\*\*  
P\_AAW85722 361 ADLNTEGMAAEKCRASTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTQD  
  
DNA40981 421 TGMYTCMVSNSVGNTTASATLNVTAATTPFSYFSTVTVETMEPSQDEARTTDNNVGPTP  
\*\*\*\*\*  
P\_AAW85722 421 TGMYTCMVSNSVGNTTASATLNVTAATTPFSYFSTVTVETMEPSQDEARTTDNNVGPTP

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BEST RESULTS B-7

DNA40981 481 VVDWETTNVTTSLPQSTRSTEKTFTIPVTDINSGIPGIDEVMKTTKIIIGCFVAITLMA  
\*\*\*\*\*  
P\_AAW85722 481 VVDWETTNVTTSLPQSTRSTEKTFTIPVTDINSGIPGIDEVMKTTKIIIGCFVAITLMA  
  
DNA40981 541 AVMLVIFYKMRKQHHRQNHHAPTRTVEIINVDEITGDTPMESHLPMPAIEHEHLNHYNS  
\*\*\*\*\*  
P\_AAW85722 541 AVMLVIFYKMRKQHHRQNHHAPTRTVEIINVDEITGDTPMESHLPMPAIEHEHLNHYNS  
  
DNA40981 601 YKSPFNHTTVNTINSIHSSVHEPLLIRMNSKDNVQETQI  
\*\*\*\*\*  
P\_AAW85722 601 YKSPFNHTTVNTINSIHSSVHEPLLIRMNSKDNVQETQI  
  
>8 P\_AAY08100 Human PRO331 protein - Homo sapiens. (640 aa) [1 seg]  
Score = 3362 (1299 bits), Expect = 0.0  
Identities = 640/640 (100%), Positives = 640/640 (100%), at 1,1-640,640  
  
DNA40981 1 MLNKMTLHPQQIMIGPRFNRALFDPLLVLALQLLVAGLVRAQTCPSVCSCSNQFSKV  
\*\*\*\*\*  
P\_AAY08100 1 MLNKMTLHPQQIMIGPRFNRALFDPLLVLALQLLVAGLVRAQTCPSVCSCSNQFSKV  
  
DNA40981 61 ICVRKNLREVPDGISTNTRLLNLHENQIQIICKVNSFKHLRHLEILQLSRNHIRTIEIGAF  
\*\*\*\*\*  
P\_AAY08100 61 ICVRKNLREVPDGISTNTRLLNLHENQIQIICKVNSFKHLRHLEILQLSRNHIRTIEIGAF  
  
DNA40981 121 NGLANLNTLELFDNRLTTIPNGAFVYLSKLKEWLRLNNPIESIPSYAFNRIPSLRRLDLG  
\*\*\*\*\*  
P\_AAY08100 121 NGLANLNTLELFDNRLTTIPNGAFVYLSKLKEWLRLNNPIESIPSYAFNRIPSLRRLDLG  
  
DNA40981 181 ELKRLSYISEGAFEGLSNLRYLNLCNLREIPNLTPLIKLDLDELSGNHLSAIRPGSFQ  
\*\*\*\*\*  
P\_AAY08100 181 ELKRLSYISEGAFEGLSNLRYLNLCNLREIPNLTPLIKLDLDELSGNHLSAIRPGSFQ  
  
DNA40981 241 GLMHLQKLWMIQSQIQVIERNADFNLQLSVEINLAHNNLTLLPHDLFTPPLHHLERIHLH  
\*\*\*\*\*  
P\_AAY08100 241 GLMHLQKLWMIQSQIQVIERNADFNLQLSVEINLAHNNLTLLPHDLFTPPLHHLERIHLH  
  
DNA40981 301 NPWCNCIDILWLSWWIKDMAPSNTACCACNTPPNLKGRYIGELDQNYFTCYAPVIVEP  
\*\*\*\*\*  
P\_AAY08100 301 NPWCNCIDILWLSWWIKDMAPSNTACCACNTPPNLKGRYIGELDQNYFTCYAPVIVEP  
  
DNA40981 361 ADLNTEGMAAEELKCRASTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVQD  
\*\*\*\*\*  
P\_AAY08100 361 ADLNTEGMAAEELKCRASTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVQD  
  
DNA40981 421 TGYTCMVSNSVGNTTASATLNTAATTPFSYFSTVTVETMEPSQDEARTTDNNVGPTP  
\*\*\*\*\*  
P\_AAY08100 421 TGYTCMVSNSVGNTTASATLNTAATTPFSYFSTVTVETMEPSQDEARTTDNNVGPTP  
  
DNA40981 481 VVDWETTNVTTSLPQSTRSTEKTFTIPVTDINSGIPGIDEVMKTTKIIIGCFVAITLMA  
\*\*\*\*\*  
P\_AAY08100 481 VVDWETTNVTTSLPQSTRSTEKTFTIPVTDINSGIPGIDEVMKTTKIIIGCFVAITLMA  
  
DNA40981 541 AVMLVIFYKMRKQHHRQNHHAPTRTVEIINVDEITGDTPMESHLPMPAIEHEHLNHYNS  
\*\*\*\*\*  
P\_AAY08100 541 AVMLVIFYKMRKQHHRQNHHAPTRTVEIINVDEITGDTPMESHLPMPAIEHEHLNHYNS  
  
DNA40981 601 YKSPFNHTTVNTINSIHSSVHEPLLIRMNSKDNVQETQI

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P\_AAY08100 601 YKSPFNHTTVNTINSIHSSVHEPLLIRMNSKDNVQETQI

>9 BAB13406.1 KIAA1580 protein - Homo sapiens (640 aa) [1 seg]

Score = 3362 (1299 bits), Expect = 0.0

Identities = 640/640 (100%), Positives = 640/640 (100%), at 1,1-640,640

DNA40981	1	MLNKMTLHPQQIMIGPRFNRALFDPLLVLLALQLVVAGLVRAQTCPSVCSCSNQFSKV
BAB13406.1	1	MLNKMTLHPQQIMIGPRFNRALFDPLLVLLALQLVVAGLVRAQTCPSVCSCSNQFSKV
DNA40981	61	ICVRKNLREVPDGISTNTRLLNLHENQIQIIKVNSFKHLRHLEILQLSRNHIRTIEIGAF
BAB13406.1	61	ICVRKNLREVPDGISTNTRLLNLHENQIQIIKVNSFKHLRHLEILQLSRNHIRTIEIGAF
DNA40981	121	NGLANLNTLELFDRNRLTTIPNGAFVYLSKLKEWLRLRNNPIESIPSYAFNRIPSLRRLDLG
BAB13406.1	121	NGLANLNTLELFDRNRLTTIPNGAFVYLSKLKEWLRLRNNPIESIPSYAFNRIPSLRRLDLG
DNA40981	181	ELKRLSYISEGAFEGLSNLRYLNLCNLREIPNLTPLIKLDELDLSGNHLSAIRPGSFQ
BAB13406.1	181	ELKRLSYISEGAFEGLSNLRYLNLCNLREIPNLTPLIKLDELDLSGNHLSAIRPGSFQ
DNA40981	241	GLMHLQKLWMIQSQIQLQVIERNADNLQLSVEINLAHNNLTLLPHDLFTPPLHHLERIHLHH
BAB13406.1	241	GLMHLQKLWMIQSQIQLQVIERNADNLQLSVEINLAHNNLTLLPHDLFTPPLHHLERIHLHH
DNA40981	301	NPWCNCIDILWLSWWIKDMAPSNTACCACNTPPNLKGRYIGELDQNYFTCYAPVIVEPP
BAB13406.1	301	NPWCNCIDILWLSWWIKDMAPSNTACCACNTPPNLKGRYIGELDQNYFTCYAPVIVEPP
DNA40981	361	ADLNTEGMAELKCRASTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVQD
BAB13406.1	361	ADLNTEGMAELKCRASTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVQD
DNA40981	421	TGMYTCMVSNSVGNTTASATLNVTAAATTTPFSYFSTVTVETMEPSQDEARTTDNNVGPTP
BAB13406.1	421	TGMYTCMVSNSVGNTTASATLNVTAAATTTPFSYFSTVTVETMEPSQDEARTTDNNVGPTP
DNA40981	481	VVDWETTNVTTSLTPQSTRSTEKTFTIPVTDINSGIPGIDEVMKTTKIIIGCFVAITLMA
BAB13406.1	481	VVDWETTNVTTSLTPQSTRSTEKTFTIPVTDINSGIPGIDEVMKTTKIIIGCFVAITLMA
DNA40981	541	AVMLVIFYKMRKQHHRQNHHAPTRTVEIINVDEITGDTPMESHLPMPAIEHEHLNHYNS
BAB13406.1	541	AVMLVIFYKMRKQHHRQNHHAPTRTVEIINVDEITGDTPMESHLPMPAIEHEHLNHYNS
DNA40981	601	YKSPFNHTTVNTINSIHSSVHEPLLIRMNSKDNVQETQI
BAB13406.1	601	YKSPFNHTTVNTINSIHSSVHEPLLIRMNSKDNVQETQI